

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2005, 16:09:56 ; Search time 32.2456 Seconds
(without alignments)
800.996 Million cell updates/sec

Title: US-09-826-791a-6
Perfect score: 1768
Sequence: 1 MERKMSLOPSTISVSEMEPN.....KAKTKCVFVSWLAKRETRV 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1779	99.5	346	4	US-09-585-876-2
2	559	31.3	337	3	US-09-044-404A-2
3	559	31.3	337	4	US-09-586-92A-2
4	483.5	27.0	339	1	US-08-153-848-44
5	483.5	27.0	339	2	US-08-812-871-3
6	483.5	27.0	339	3	US-09-299-843A-44
7	483.5	27.0	339	4	US-09-088-337B-44
8	483.5	27.0	339	3	US-09-170-496D-32
9	483.5	27.0	339	5	PCT-US83-11153-44
10	483.5	27.0	339	5	PCT-US95-07180-2
11	480.5	26.9	339	4	US-09-170-496D-182
12	464	26.0	362	3	US-08-513-974B-374
13	447.5	25.0	370	3	US-08-781-250-2
14	446	24.9	373	4	US-09-745-842-14
15	442	24.7	373	2	US-08-559-524A-4
16	442	24.7	373	3	US-08-749-707-4
17	442	24.7	373	1	US-09-947-922-4
18	440	24.6	361	4	US-08-833-750-4
19	440	24.6	361	3	US-08-352-678-4
20	440	24.6	361	4	US-09-536-954-4
21	440	24.6	361	4	US-09-170-496D-78
22	440	24.6	361	4	US-09-829-583B-4
23	440	24.6	361	5	PCT-US93-09636-4
24	439.5	24.6	348	3	US-08-852-824-17
25	439	24.6	302	2	US-08-467-948A-30
26	439	24.6	302	3	US-08-467-947A-30
27	437	24.4	344	2	US-08-467-948A-8

28	437	24.4	344	3	US-08-467-947A-8	Sequence 8, Appl1
29	434	24.3	361	4	US-09-170-496D-206	Sequence 206, App
30	434	24.3	377	4	US-09-745-842-17	Sequence 17, Appl
31	424.5	23.7	374	4	US-09-745-842-15	Sequence 15, Appl
32	419.5	23.5	373	4	US-08-513-974B-373	Sequence 373, App
33	419.5	23.5	374	3	US-09-102-710B-3	Sequence 9, Appl1
34	416	23.3	342	1	US-08-988-876-9	Sequence 2, Appl1
35	416	23.3	375	1	US-08-442-134A-2	Sequence 2, Appl1
36	416	23.3	375	1	US-08-444-581B-2	Sequence 2, Appl1
37	416	23.3	375	1	US-08-446-088A-2	Sequence 2, Appl1
38	416	23.3	375	2	US-08-559-524A-3	Sequence 3, Appl1
39	416	23.3	375	3	US-08-749-707-3	Sequence 3, Appl1
40	416	23.3	375	4	US-09-947-922-3	Sequence 3, Appl1
41	409.5	22.9	342	4	US-09-054-272-2	Sequence 2, Appl1
42	406.5	22.7	398	1	US-08-097-938-6	Sequence 6, Appl1
43	406.5	22.7	398	1	US-08-476-000-6	Sequence 6, Appl1
44	406.5	22.7	398	1	US-08-472-840-6	Sequence 6, Appl1
45	406.5	22.7	398	2	US-08-476-976-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-585-876-2
Sequence 2, Application US/09585876
Patent No. 6586205
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Siles-Santiago, Immaculada
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-like Molecule and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 5800-88
CURRENT APPLICATION NUMBER: US/09/585, 876
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/182,061
EARLIER FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-585-876-2

Query Match 99.5%; Score 1779; DB 4; Length 346;
Best Local Similarity 99.4%; Pred. No. 3.9e-131;
Matches 344; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MERKMSLOPSTISVSEMEPNNGTFSNNNSRNCITENFKREFPIVYIIIFFGVGLNGLSI	60
DB	1	MERKMSLOPSTISVSEMEPNNGTFSNNNSRNCITENFKREFPIVYIIIFFGVGLNGLSI	60
QY	61	YFLLPYKYSTSVNFMNLAIISDLFISTLPFRADYVYRGSNMWIPGDLACRIMSYSLVY	120
DB	61	YFLLPYKYSTSVNFMNLAIISDLFISTLPFRADYVYRGSNMWIPGDLACRIMSYSLVY	120
QY	121	NMYSSYFLTVLSVVRFLAMVHPFRLVHTSIRSAMILOGIIMILIMASSIMLDSGSBQ	180
DB	121	NMYSSYFLTVLSVVRFLAMVHPFRLVHTSIRSAMILOGIIMILIMASSIMLDSGSBQ	180
QY	181	NGSVTSCLELNKYKAKQTMNYIALVVGCLLPFFLSICYLLIRVLAKVEPESGLRV	240
DB	181	NGSVTSCLELNKYKAKQTMNYIALVVGCLLPFFLSICYLLIRVLAKVEPESGLRV	240
QY	241	SHRKALTTITITLIFLFCFLPYHTLRTHLTVMKVGCKDRHLKALVTITLALANAGP	300
DB	241	SHRKALTTITITLIFLFCFLPYHTLRTHLTVMKVGCKDRHLKALVTITLALANAGP	300
QY	301	NFLVYFAGENFKDRLSALRGHPQAKTKCVFVSWLAKRETRV	346
DB	301	NFLVYFAGENFKDRLSALRGHPQAKTKCVFVSWLAKRETRV	346

```

US-09-044-404A-2      RESULT 2
; Sequence 2, Application US/09044404A
; Patent No. 6200775
; GENERAL INFORMATION:
; APPLICANT: SATHI, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: JAMES, ROBERT
; APPLICANT: FOLEY, JAMES
; APPLICANT: SARAU, HENRY
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 790 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,404A
; FILING DATE: MARCH 19, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,795
; FILING DATE: APRIL 22, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T.
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH-70001-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-044-404A-2
;
Query Match          31.3%; Score 559; DB 3; Length 337;
Best Local Similarity 38.0%; Pred. NO. 3.8e-36;
Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7
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QY 27 NSRNC--TIENFKREFPIVLLIIFWGVLAGSLIYVFLQPYKSTSVNFMNLATSD 84
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 SSATCHPTIDDFRNQVSTLYKSMISVGFPGNGFVLYLIKTIYHKKSAPQYMMILAVAD 69
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 85 LLFSTLPFRADYTIIRGSNMIIFGLACINISLYVNMSSITFLTVLSVRFAMVHPF 144
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 LLCCTLPRLRVVYVYHKGIWFGDFLCRLSTVALVYNLYCSIFFTWAMSPFCIAIVPV 129
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 145 RLHVTISRSMILICGIMI-LIMASSIMLLDSGSEQNGSVTSCLEMLYKAK--LQTM 201
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 QNIVLVQKQKAPFCVGMIVILTSSEFLMAKPKQSGKNNKTCPEPPQDNQTKNHLVL 189
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 202 NYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIFLCFL 261
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 HYVALFPGFIIFPVIIIVCYTMITILTKKSMKKN--LSHKKALGMIMVTAFLVSEFM 247
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 262 PYHILRVVHLTTM--KYGCLCD--RLHKAIVTTLAALAAACPNLDLYYFAGENFKDLK 317
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db      248 PPHIORTIHLFHNHETKPCDSVLHMQSGSVITLTLAASNCDFDLVFFSGNFRRKL- 306
Qy      318 SALRK 322
        |||
Db      307 STFRK 311

RESULT 3
US-09-586-924-2
; Sequence 2, Application US/09586924
; Patent No. 6506878
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH M.
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: AMES, ROBERT S.
; APPLICANT: FOLEY, JAMES U.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: CHAMBERS, JON
; TITLE OF INVENTION: CDNA CLONE HMTWFB1 THAT ENCODES A NOVEL
; TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
; FILE REFERENCE: GH-70001-1D1
; CURRENT APPLICATION NUMBER: US/09/586,924
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 09/044,404
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/844,795
; PRIOR FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-586-924-2

Query Match      31.3%; Score 559; DB 4; Length 337;
Beet Local Similarity 38.0%; Pred. No. 3.8e-36;
Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;

Qy      27 NSRNC--TIENPKKEFPPIYVLIIFPGVLGNGLSIYVFLDPYKSTSVNFMNLAIKD 84
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      10 SSAATCHDITIDFRNQVYSTLYSMISVVGFGNGFVLVLKTHYKKAFOYMYMNLAVAD 69
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      85 LLEFSTLPEFRADYYLKRSGNWIFGDLACRINSYSLYVNMYSIYVLTVLSVFRFLAMVHPF 144
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      70 LLCTCTPLRVRVYVYVHGMIMLFCDPLCRSLSTYALYNMLCSIFPMTAMSFRCIAIVPV 129
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      145 RLHVTSGRSAMWILCGIWI--LIWASSIMLLDSSGDSGVSITGLEINIVKAK--LQTM 201
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      130 QNINLVYOKKARFVCGVGMIFVILITSSPFLMAKPOKQGNNTKCEPPODNQTNHVLVL 189
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      202 NYIALVVGCLLPFTLISYVLLIIRVLLAKYVEPSGHRVSHRKALTYIIITLLIFPLCL 261
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      190 HYVELFVGFIIPFTIILVCTMTIILTLKKSMKN--LSHKKAKALIGIMVYTAFLVSFM 247
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      262 PYHTRIVVHITTW--KVGCLKD--RLHKAIVITLALAANAACFNPLIYYAGENFKORLK 317
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      248 PYHQRTHLHFLHNHETKPCDSVLRMQSGSVITLTLAASNCDFDLVFFSGGFRRL- 306
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      318 SALRK 322
        |||
Db      307 STFRK 311

RESULT 4
US-08-153-848-44
; Sequence 44, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.

```

TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Garstelein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-44

Query Match 27.0%; Score 483.5; DB 1; Length 339;
Best Local Similarity 34.6%; Pred. No. 2,9e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

QY 16 EMEPNG---TFSNNNSRNCTIEN-FKRBEFPVLYLIIFFMVGLNGLSIYVFLQPKKST 71
DB 5 EVAPRGILTNFSLATAEQQGQETPLENMLFASFYLLDFTLALVGNLTALMLFIRHKSQT 64
QY 72 SVNVFMLNLAISDLIFSTLPPRADYYLRGSNWIFGDLACRIMSYSLVYNNMTSSIFYLTV 131
DB 65 PANVFLMLHVAVDLSCVVLPTRLVYHFGSNHWPGEIACRLTGLFYLMYASIFYLTC 124
QY 132 LSVNPLMANVHPRRLHNTSIRSAWILCGIWIILI-MASSIMLDSGSRGNSVTSCLBL 190
DB 125 ISADRFLLAIHVHVKSLKRLRPYAHDLACFLWVVAAPRLVSPQVQTNHTVVCLO- 183
QY 191 NLYKAKLQTNMYIALVVGCLLPFFTLSCYLLIIRVLKVEVPSGLVSHR---KALT 247
DB 184 -LYR-EKSHNALVELAFAFTFPITTYTCYLLIIRSL-----RGLRVERKRLTKAVR 235
QY 248 TTIITLIIFLCLPPLHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANCFNPL 303
DB 236 MIAIVLAIFLVCFVPHVNRVYVLYHRSHGASCATQRIALANRITSCITSLNGALDPI 295
QY 304 LYYFAGENFKDRLSKAL---RKGHPQAKTK 331
DB 296 MYFVAEKFRHALCNLCCGKRLGPPSPBEGK 327

RESULT 5
US-08-812-871-3
Sequence 3, Application US/08812871
Patent No. 5955303
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice

APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 992700
US-08-812-871-3

Query Match 27.0%; Score 483.5; DB 2; Length 339;
Best Local Similarity 34.6%; Pred. No. 2,9e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

QY 16 EMEPNG---TFSNNNSRNCTIEN-FKRBEFPVLYLIIFFMVGLNGLSIYVFLQPKKST 71
DB 5 EVAPRGILTNFSLATAEQQGQETPLENMLFASFYLLDFTLALVGNLTALMLFIRHKSQT 64
QY 72 SVNVFMLNLAISDLIFSTLPPRADYYLRGSNWIFGDLACRIMSYSLVYNNMTSSIFYLTV 131
DB 65 PANVFLMLHVAVDLSCVVLPTRLVYHFGSNHWPGEIACRLTGLFYLMYASIFYLTC 124
QY 132 LSVNPLMANVHPRRLHNTSIRSAWILCGIWIILI-MASSIMLDSGSRGNSVTSCLBL 190
DB 125 ISADRFLLAIHVHVKSLKRLRPYAHDLACFLWVVAAPRLVSPQVQTNHTVVCLO- 183
QY 191 NLYKAKLQTNMYIALVVGCLLPFFTLSCYLLIIRVLKVEVPSGLVSHR---KALT 247
DB 184 -LYR-EKSHNALVELAFAFTFPITTYTCYLLIIRSL-----RGLRVERKRLTKAVR 235
QY 248 TTIITLIIFLCLPPLHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANCFNPL 303
DB 236 MIAIVLAIFLVCFVPHVNRVYVLYHRSHGASCATQRIALANRITSCITSLNGALDPI 295
QY 304 LYYFAGENFKDRLSKAL---RKGHPQAKTK 331
DB 296 MYFVAEKFRHALCNLCCGKRLGPPSPBEGK 327

RESULT 6
US-09-299-843A-44

Db 184 -LYR-EKASHNALVSLAVAFTEPFTTTCYLLIIRSL-----RQGLVERKRLTKAVR 235
 Qy 248 TTTTTLTLPFLGFLPHTLTATVHLTTWKY--GLCKDRHLKALV--ITLALAAANACFNPJ 303
 Db 236 MIAIVLAIFLVCFVPRVHVRSYVVLHYRSHGASCATQRIALANRITSCITSLNGALDPI 295
 Qy 304 LYYFAGENFKDRKLSAL-----RKGHPOKAKTK 331
 Db 296 MYFVAEKFRHALCNLLCGKRLKGPPSPBEGK 327

RESULT 8 US-09-170-496D-32

/ Sequence 32, Application US/09170496D
 / Patent No. 6555339
 / GENERAL INFORMATION:
 / APPLICANT: Behan, Dominic P.
 / APPLICANT: Chalmers, Derek T.
 / APPLICANT: Liaw, Chen W.
 / TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
 / TITLE OF INVENTION: Receptor
 / FILE REFERENCE: AREN-0040
 / CURRENT APPLICATION NUMBER: US/09/170,496D
 / CURRENT FILING DATE: 1998-10-13
 / NUMBER OF SEQ ID NOS: 294
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 32
 / LENGTH: 339
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-170-496D-32

Query Match 27.0%; Score 483.5; DB 4; Length 339;
 Best Local Similarity 34.6%; Pred. No. 2.9e-30;

Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

Qy 16 EMEPRG---TFSNNNSRNTIEN-FKREPRPIVYLIIFFWGVLGNGLSIVFLQPKKST 71
 Db 5 EVAPRGLITNFSLATBEOGQETPLENMLFASFYLLDFITALVGNLTALMLPFRDHSKT 64
 Qy 72 SVNVFMLNLAIDLLPFIPTPRADYLLRGSNMIFGDLACRIMSYSLYVMYSSIVFLTV 131
 Db 65 PANVFLMHLAVADLSCVLVLPRLVYHBSGNMPPGEIACRLGLPFIYLMASIVFLTC 124
 Qy 132 LSVRFPLANVHPRLIHTYSIRSAWILCGIWIIL-MASSIMLDGSSQNGSVTSCLEL 190
 Db 125 ISADRFIAIVHVKSLKRLRPYAHLCAPFLWVVAVAMAPLLVSPQVQTNHTVVCLO- 183
 Qy 191 NLYKIAKIQTMNYIALVVGCLLPFTLSICYLIIIRVLKVEVPBSGLAVSHR---KALT 247
 Db 184 -LYR-EKASHNALVSLAVAFTEPFTTTCYLLIIRSL-----RQGLVERKRLTKAVR 235
 Qy 248 TTTTTLTLPFLGFLPHTLTATVHLTTWKY--GLCKDRHLKALV--ITLALAAANACFNPJ 303
 Db 236 MIAIVLAIFLVCFVPRVHVRSYVVLHYRSHGASCATQRIALANRITSCITSLNGALDPI 295
 Qy 304 LYYFAGENFKDRKLSAL-----RKGHPOKAKTK 331
 Db 296 MYFVAEKFRHALCNLLCGKRLKGPPSPBEGK 327

RESULT 9 PCT-US93-11153-44

/ Sequence 44, Application PC/TUS9311153
 / GENERAL INFORMATION:
 / APPLICANT: Godiska, Ronald
 / APPLICANT: Gray, Patrick W.
 / APPLICANT: Schmelkart, Vicki L.
 / TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 / NUMBER OF SEQUENCES: 64
 / CORRESPONDENCE ADDRESSES:
 / ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 / ADDRESSEE: Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
 STATE: Illinois
 COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/11153
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448

TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: protein

PCT-US93-11153-44

Query Match 27.0%; Score 483.5; DB 5; Length 339;
 Best Local Similarity 34.6%; Pred. No. 2.9e-30;

Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

Qy 16 EMEPRG---TFSNNNSRNTIEN-FKREPRPIVYLIIFFWGVLGNGLSIVFLQPKKST 71
 Db 5 EVAPRGLITNFSLATBEOGQETPLENMLFASFYLLDFITALVGNLTALMLPFRDHSKT 64
 Qy 72 SVNVFMLNLAIDLLPFIPTPRADYLLRGSNMIFGDLACRIMSYSLYVMYSSIVFLTV 131
 Db 65 PANVFLMHLAVADLSCVLVLPRLVYHBSGNMPPGEIACRLGLPFIYLMASIVFLTC 124
 Qy 132 LSVRFPLANVHPRLIHTYSIRSAWILCGIWIIL-MASSIMLDGSSQNGSVTSCLEL 190
 Db 125 ISADRFIAIVHVKSLKRLRPYAHLCAPFLWVVAVAMAPLLVSPQVQTNHTVVCLO- 183
 Qy 191 NLYKIAKIQTMNYIALVVGCLLPFTLSICYLIIIRVLKVEVPBSGLAVSHR---KALT 247
 Db 184 -LYR-EKASHNALVSLAVAFTEPFTTTCYLLIIRSL-----RQGLVERKRLTKAVR 235
 Qy 248 TTTTTLTLPFLGFLPHTLTATVHLTTWKY--GLCKDRHLKALV--ITLALAAANACFNPJ 303
 Db 236 MIAIVLAIFLVCFVPRVHVRSYVVLHYRSHGASCATQRIALANRITSCITSLNGALDPI 295
 Qy 304 LYYFAGENFKDRKLSAL-----RKGHPOKAKTK 331
 Db 296 MYFVAEKFRHALCNLLCGKRLKGPPSPBEGK 327

RESULT 10 PCT-US95-07180-2

/ Sequence 2, Application PC/TUS9507180
 / GENERAL INFORMATION:
 / APPLICANT: LI, YI
 / APPLICANT: GOCAYNE, JEANINE D
 / APPLICANT: ROSEN, STEVEN M
 / TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBB69
 / NUMBER OF SEQUENCES: 9
 / CORRESPONDENCE ADDRESSES:
 / ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

ADDRESSEE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NJ
COUNTRY: US
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07180-2

Query Match 27.0%; Score 483.5; DB 5; Length 339;
Best Local Similarity 34.6%; Pred. No. 2,9e-30;

Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

QY 16 EMEPNQ---TFSNNNSRNTIEN-FKREPPPIVYLIIFFWGVINGLSIVFLQPYKKSST 71
DB 5 EVAPBGLITNFSLATBEOCGQETPLBNMLFASFYLLDFILATVGNLTALMLFIRHKSST 64
QY 72 SVNVFMLNLAISDLPLFISTLPPRADYYLNGSNWIFGDLACRIMSYSLYNNMYSIYFLTV 131
DB 65 PANVFMLHLAVADLSCVLPFLVYHFGSNHMPFGELACRLTGFLFYLMVYASIFPLTC 124
QY 132 LSVRFLMVAHPRLIHTSIRSAMTLCGIITWLI-MASIMLDGSGEONGSVTSCLEL 190
DB 125 ISADRFIAIVHPVKSILKRRPLVAHLACAFIMVVAVMAAPLVSQVQTQNTHTVVCLO- 183
QY 191 NUYKIACLQTMNYIALVVGCLPFFTLSTCYLLIIRVLLKVEVPBSGLRVSHR---KALT 247
DB 184 -LYR-EKASHNALVSLAFAFTFPFITVTCYLLIIRSL-----ROGLRVERKRLTKAKR 235
QY 248 TIIITLIIFFLCPLPYHTLRTVHLTTWKV--GLCKDRHLKALV--ITLALAANCFNPL 303
DB 236 MAIVAIATFLVCFVPHVNRSVYVLYHRSHGASCATQRIILANRITSCLTSLNGALDPI 295
QY 304 LYVPAGENPKRLKSL-----RKGNPQAKTK 331
DB 296 MYFVAEKFRHALCNLLCGKRLKGPSPSEK 327

RESULT 11

US-09-170-496D-182
Sequence 182, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294

SOFTWARE: Patentin version 3.1
SEQ ID NO 182
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-170-496D-182

Query Match 26.9%; Score 480.5; DB 4; Length 339;
Best Local Similarity 34.6%; Pred. No. 5e-30;

Matches 115; Conservative 62; Mismatches 130; Indels 25; Gaps 10;

QY 16 EMEPNQ---TFSNNNSRNTIEN-FKREPPPIVYLIIFFWGVINGLSIVFLQPYKKSST 71
DB 5 EVAPBGLITNFSLATBEOCGQETPLBNMLFASFYLLDFILATVGNLTALMLFIRHKSST 64
QY 72 SVNVFMLNLAISDLPLFISTLPPRADYYLNGSNWIFGDLACRIMSYSLYNNMYSIYFLTV 131
DB 65 PANVFMLHLAVADLSCVLPFLVYHFGSNHMPFGELACRLTGFLFYLMVYASIFPLTC 124
QY 132 LSVRFLMVAHPRLIHTSIRSAMTLCGIITWLI-MASIMLDGSGEONGSVTSCLEL 190
DB 125 ISADRFIAIVHPVKSILKRRPLVAHLACAFIMVVAVMAAPLVSQVQTQNTHTVVCLO- 183
QY 191 NUYKIACLQTMNYIALVVGCLPFFTLSTCYLLIIRVLLKVEVPBSGLRVSHR---KALT 247
DB 184 -LYR-EKASHNALVSLAFAFTFPFITVTCYLLIIRSL-----ROGLRVERKRLTKAKR 235
QY 248 TIIITLIIFFLCPLPYHTLRTVHLTTWKV--GLCKDRHLKALV--ITLALAANCFNPL 303
DB 236 MAIVAIATFLVCFVPHVNRSVYVLYHRSHGASCATQRIILANRITSCLTSLNGALDPI 295
QY 304 LYVPAGENPKRLKSL-----RKGNPQAKTK 331
DB 296 MYFVAEKFRHALCNLLCGKRLKGPSPSEK 327

RESULT 12

US-08-513-974B-374
Sequence 374, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:

Query Match	24.4%	Score 436	DB 2	Length 344
Best Local Similarity	32.0%	Pred. No. 3.4e-28		
Matches 98	Conservative 73	Mismatches 113	Indels 22	Gaps 8

[illegible]

QY 146 LHVATSRSAWILCGIILWILM--ASSIMLLDGSSEONGSVTSCLEINLYKIAKLTQTN 202
 Db 124 SKIITRTKRNAAIVCTGVMWLVIGSAPAVFQSTHSQGNNAASACFE-NPEEATMKYLS 182
 QY 203 YIAL---VGCGLPEPTLTSTCYLLIRKLVKVEBPESGLRSHKALTTITITITIFPLC 259
 Db 183 RIVFIEIVGRFIPILINVTSSMVLKTLTK-PYTLSSRSKINKTKVLMIPVHILIECFQ 241

[illegible]

RESULT 8
A47556
ATP receptor P2u - mouse
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: A47556
R/Justify, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A/Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A/Reference number: A47556; MUID:93281707; PMID:7685114
A/Accession: A47556
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1373 <LUS>
A/Cross-references: UNIPROT:P35383; GB:U14751; NID:g309457; PIND:AAA9871.1; PID:g309458
C/Superfamily: ATP receptor P2u
C/Keywords: transmembrane protein

Query Match	23.6%	Score 421.5;	DB 2;	Length 373;
Best Local Similarity	31.6%;	Pred. No. 5.6e-27;		
Matches 106;	Conservative	99;	Mismatches 131;	Indels 29;
			Gaps	10;

```
QY      15 SEMEP-----NGTFSSNN-SRNCTI-ENFKREFPPIVLLIFFWGLGNGLSIVFLOPY 67
        ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

RESULT 9

```

RESULT 9
S13638
Platelet-activating factor receptor - guinea pig
C/Species: Cavia porcellus (guinea pig)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S13638
R/Honda, Z.; Nakamura, M.; Maki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; Toi
Nature 349, 342-346, 1991
A/Title: Cloning by functional expression of platelet-activating factor receptor from guinea
A/Reference number: S13638; WUID:91101726; PMID:1846531
A/Accession: S13638
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-342 <HON>
A/Cross-references: UNIPROT:P21566; GBX:X6736; NID:q94942; PIRN:CAA0060.1; PID:q94943
A/Note: the species of guinea pig is not identified; in GenBank entry CCFAPREC, release 1
A/Superfamily: ATP receptor p2u

```

Query Match 23.3%; Score 416; DB 2; Length 342;
Best Local Similarity 30.4%; Pred. No. 1.4e-26;
Matches 97; Conservative 67; Mismatches 137; Indels 18; Gaps 7

Query Match 23.3%; Score 416; DB 2; Length 342;
Best Local Similarity 30.4%; Pred. No. 1.4e-26;
Matches 97; Conservative 67; Mismatches 137; Indels 18; Gaps 7

Qy 27 NSRNCITENFKKEFFPIVYLIIFFWGLGNGLSIYVF--LQPKKSTSVNVEMNLALSD 84
||:|||||||::||::|||:||||:|
Db 4 NSSSRVDSEFRYLFPPIVYSIIIFVLGIANGYLMVBARLYBSKKLNEIKIEMVNLTVAD 63

85 LIFISTIPERADYYLRGSNWIFGDLACRIMSYSLYNNYSSIELTVLSVREFLAMVHPF 144

D6 64 LLEFLITPLPMIYYSSNGSNMFLPKFLCNLAGCLFFINTYCSVAFLGVIITNRFQAVKYEI 123

OY 145 RLHHTVSIRSAMILCGIIMILM--ASSIMLMD-----SGSEONGSVTSCLEINLYKIAK 197

Db 124 KTAQATTRKRGIALLSLVIWVALVAABSYFLVNDSTNVVSNKAGSGNTRCFE-HYEKSGK 182

Dy 198 LQTMNIALVWGCLLPFTLSICYLLIRVLKVEYEGSLVSHRKALTTIIITLIFP 257
::|:|:|:|:|:|:|:|:|:|:
Db 183 PVLIIHICIVAGFFIVFLLEFCNLVIHTLRQPVAQQRNAEVRRLIMVCVLAVEFV 242

258 I C E L P Y H T L R T V H L T T W K V G L C K D R L H K A L ----- V I T L A A A N A C F N D L Y Y F A G E N F K 313

DB 243 ICFVPHHVVQ-LPWILAEALGWMPSNNQAINDAHQVITLCILSTINCVDLPVLYCFETKKER 301

QY 314 DRLKSAIRKGHPQAKTYC 332

Db 302 KHLSEK---NIMRSSQKC 317

RESULT 10
A54946
P-2U nucleotide receptor - human

C:\Species: Homo sapiens (man)
C:\Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1995
C:\Accession: A54946
P:\Part, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994
A:\Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic
A:\Reference number: A54946; MUID:94211846; PMID:8159738
A:\Accession: A54946
A:\Status: Preliminary
A:\Molecule type: mRNA, protein
A:\Residues: 1-375 <PAR>
A:\Cross-references: GB:U07225
A:\Note: parts of this sequence were confirmed by protein sequencing
C:\GeneticB:
A:\Gene: GDB:P2RY2, HP2U, P2U
A:\Cross-references: GDB:362713; OMIM:60041
A:\Map position: 11q13.5-11q14.1
C:\Superfamily: ATP receptor P2u
C:\Keywords: G protein-coupled receptor; transmembrane protein

Query Match 23.3%, Score 416, DB 2, Length 375;
Best Local Similarity 31.6%, Pred. No. 1,6e-26;
Matches 100, Conservative 67, Mismatches 131, Indels 18, Gaps 8;

Qy 20 NGTGSNN-SNCTI-ENKREFPPIVYLLIFPGVLANGSIYFLOPKKTSNVEM 77
Db 13 NGTWDBELGYRCRPNEDFKYVLLPVSXGVCVLGLCNAAVGLYIFLCRLTWNASTYM 72
Qy 78 LNLAIIDLPISTPFRADYLLRGSNNWIFGDLACRINSYSLYNMYSIYFVLTLSVRF 137
Db 73 PHLAVSDALVAASPLVLYYARGDHMFSTVLCVAFLEFYTNLYCSILPLTICSHRC 132
Qy 138 LAMVHPPELLVHTSIRSAMILGIIWILIMASSIMLDSGSEQNGSVTSCLEMLYKIAK 197
Db 133 LGVLRPLRSLSKMGARAYARVAGAVVVLVLAQAPVLFVTTSAKGLPITCHDSAPELFS 192
Qy 198 LQTMNYIALVVGCL-LPFTLSICILYILITVLLKVEPES-GRVSHKALTYITLI 254
Db 193 -RFAVASYSVMIGLLFAVPFAVILVCCYVLMARLLKPAVGTSGGPPRAKRSVRTIAVLA 251
Qy 255 IFFLCFPIPYHILRTVHLJTTWKVGLCKDRHLKALVITLA-----LAAANACFNPILYYFAG 309
Db 252 VFALCFDPFHVTRTRLYYSFRSLD---SCHTLAIAINMAKYKTRILASANSCLDPVLYFLAG 308
Qy 310 ENFDRRLKSALRKGP 325
Db 309 Q----RLVRPARDAKP 320

RESULT 11
A40191
platelet-activating factor receptor - human
C:\Species: Homo sapiens (man)
C:\Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
C:\Accession: A40191, JH0479, A41079, JCI359, A42831, I51923
P:\Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A:\Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell
A:\Reference number: A40191; MUID:92250505; PMID:1374385
A:\Accession: A40191
A:\Molecule type: mRNA
A:\Residues: 1-342 <KUN>
A:\Cross-references: UNIPROT:P25105; GB:M76674; NID:G456293; PID:AAA60001.1; PID:G456294
R:\Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochran, C.G.
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A:\Title: Characterization of a human cDNA that encodes a functional receptor for platelet
A:\Reference number: JH0479; MUID:92028922; PMID:1656963
A:\Accession: JH0479
A:\Molecule type: mRNA
A:\Residues: 1-342 <YER>
A:\Cross-references: GB:M60436; NID:G189537; PID:AAA60001.1; PID:G189538
A:\Experimental source: granulocyte, cell line HL-60 all
P:\Nakamura, M.; Honda, Z.; Izumi, T.; Sakenaka, C.; Mutoh, H.; Minami, M.; Bito, H.; Sey

J. Biol. Chem. 266, 20400-20405, 1991

At1Title: Molecular cloning and expression of platelet-activating factor receptor from human platelets

A1Accession: A41079

A1Status: not compared with conceptual translation

A1Molecule type: mRNA

A1Residues: 1-342 <NA>

A1Cross-references: GB:DI0202; GB:D90433; NID:g219975; PIDN:BA01050.1; PID:g219976

R1Symptom: T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y.

B1Biochem. Biophys. Res. Commun. 189, 617-624, 1992

At1Title: Molecular cloning and characterization of the platelet-activating factor receptor

A1Reference number: JCI359; MUID:93112021; PMID:1281995

A1Accession: JCI359

A1Molecule type: mRNA

A1Residues: 1-315, 'N', 317-342 <SUG>

A1Experimental source: heart

A1Note: The authors translated the codon AAT for residue 316 as Lys

R1Seiyfried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.

Genomic 13, 832-834, 1992

At1Title: The human platelet-activating factor receptor gene (P1A1FR) contains no introns

A1Reference number: A42831; MUID:92347886; PMID:1322356

A1Accession: A42831

A1Molecule type: DNA

A1Residues: 1-326, 'TG', 229-342 <SEV>

A1Cross-references: GB:M88177; NID:g190697; PIDN:AAA0214.1; PID:g190698

A1Note: Sequence extracted from NCBI backbone (NCBIN:109813, NCBI:P.109814)

R1Chase, P.B.; Halonen, M.; Regan, J.W.

Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

At1Title: Cloning of a human platelet-activating factor receptor gene: evidence for an intron

A1Reference number: I51923; MUID:93192035; PMID:8383507

A1Accession: I51923

A1Status: preliminary; translated from GB/EMBL/DBJ

A1Molecule type: DNA

A1Residues: 1-342 <RES>

A1Cross-references: GB:S56396; NID:g298580; PIDN:AA85755.1; PID:g298581

C1Genetics:

A1Gene: GDB:P1A1FR

A1Cross-references: GDB:128806; OMIM:173393

A1Map position: 1p35-1p34.3

C1Superfamily: ATP receptor P2U

C1Keywords: G protein-coupled receptor; transmembrane protein

P117-38/Domain: transmembrane #status predicted <TRI>

P154-75/Domain: transmembrane #status predicted <TII>

P192-113/Domain: transmembrane #status predicted <TII>

P1134-155/Domain: transmembrane #status predicted <TIV>

P1184-205/Domain: transmembrane #status predicted <TV>

P1233-253/Domain: transmembrane #status predicted <TVI>

P1277-257/Domain: transmembrane #status predicted <TVII>

Query Match 22.9%; Score 409.5; DB 2; Length 342;

Best Local Similarity 31.3%; Pred. No. 4.9e-26;

Matches 103; Conservative 64; Mismatches 137; Indels 25; Gaps 9;

17 MEPNGTSNNNSRNCITENFKREFFPIYVLIIFPMGVNLGSLIYF--LQPIKSKTSVN 74

1 MEHPDS-SHMS-----EPRYLPRPIVYSIFVLGVIANGYLWVFARLYPCKKFEIK 53

75 VFMNLALSDLLFISTLPFRADYLRGSMWIFGDLACRMSYSLYNMTYSIYFLTVLSV 134

54 IFPNVLTNADMLFLLTLPRLMVIYVYONQGMILPKFLCNVAGCLFFINTYCSVFLGVITY 113

135 VRFLAMVHPRLNLHTSIRSAMILGCIWILIM--ASSIMLDS-----GSEONGSVTSC 187

114 NRFOAVTRPIKTAQNTKRKRGISLSTLVIMVALVGAASYFLIDSTNTVPDSAGSNVTRC 173

188 LELNLTKAKIQTMMYIALVVGCLLPFTLSICYLIIIVLAKVEVPSGLRVSRRKALT 247

174 FE-HYEKSSVPLLIHIFIVSFPLVFLILFCNVIITLTLQMPVQOQRNMEVKKRALW 232

248 TIITTLIFPCLFPLHYHLRTVHLTTWKVGLCKDRLRHKL-----VTLTLAANACFNPL 303

233 MCVTVLAVFIICFVPHHVVQ-LPMTLAEIGFODSKFHQINAHQVTLCLSLNCVLDPV 251

QY 304 LYYFAGENFDRRLKSAALRKGHPQAKTKC 332
 DB 292 IYCFELTKKFR---KHLEKFKYSMRSSRKC 317

RESULT 12

151667
 thrombin receptor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: I51667
 R:Derstzen, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevich, T.; Turck, C.W.; Vu, T.H.; C
 Nature 368, 648-651, 1994
 A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac
 A:Reference number: I51667; MUID:94195429; PMID:8145852
 A:Accession: I51667
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-420 <GBR>
 A:Cross-references: UNIPROT:P47749; EMBL:U09632; NID:G495197; PIDN:AAA18498.1; PID:G4951

Query Match

Best Local Similarity 22.7%; Score 406; DB 2; Length 420;
 Best Local Similarity 30.9%; Pred. No. 1.2e-25;
 Matches 102; Conservative 66; Mismatches 128; Indels 34; Gaps 7;

QY 16 EMBPNGTFSSNNNS-----RQCTIE-----NFKREFFPIVYLIIFFMGVLGNG 57
 DB 61 ELDESEGGSDQAPVRSARKPRRNTITKAEQYLSQWLTKEVPSIYVFIYVGLPLML 120
 QY 58 LSIYVFLQPYKSTSVNVFNLALISDLLEISTLPFRADYLRKSNWIFGDLACRIMSYA 117
 DB 121 LAIIIFLPKKKRVKPAVVVWNLALADVFVSVLPFKIAVHLSGNDMLRGPCKRITVTAI 180
 QY 118 LYNNMTSSIFYELTVLSVFRPLAVNHPRLHNTSISAWLIGIIMILMASSIMLDSG 177
 DB 181 FPCNMTCVSYLLIASISVDREPLAVVPMHSLSMRTMSRAVMACSFIMLISASTIPPLVTE 240
 QY 178 SEO---NGVSTGLENLKYIALQIMNYIALVVGCL----PEFTLSICYLLIIRVLAK 230
 DB 241 QYQKIRLDITTHDVLDKDLKDFIYFSSR--CLLFFPVFIITTCYIGIISLS 298
 QY 231 VEVPSGLRVSHRKALTTIIITLIFELPPLRYHTLRVHLTTWKVGLCKDRILHKLAVT 290
 DB 299 SSLENS---CKKTRALFLAVVLCVFLIGCPITNVFLTHY----LQANEPFIYFAYILS 351
 QY 291 LALAAANACPNPLIYFAGENFDRRLKSAAL 320
 DB 352 ACVGSVSCCLDPLIYYAASQCCORLYYSLL 381

RESULT 13

563666
 platelet activating factor receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S63666
 R:Ishii, S.; Matcunda, Y.; Nakamura, M.; Waga, I.; Kame, K.; Izumi, T.; Shimizu, T.
 Biochem. J. 314, 671-678, 1996
 A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localiz
 A:Reference number: S63666; MUID:96239129; PMID:8670084
 A:Accession: S63666
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-341 <LSH>
 A:Cross-references: UNIPROT:Q62035; EMBL:D50872; NID:G1256924; PIDN:BAA09468.1; PID:G125
 C:Superfamily: ATP receptor P2u

Query Match

Best Local Similarity 22.6%; Score 404; DB 2; Length 341;
 Best Local Similarity 30.5%; Pred. No. 1.4e-25;
 Matches 101; Conservative 66; Mismatches 134; Indels 30; Gaps 10;

QY 17 MBPNGTFSSNNNSRNTIENFKREFFPIVYLIIFFMGVLGNGLSIYV--LQPYKSTSVN 74
 DB 17 MBPNGTFSSNNNSRNTIENFKREFFPIVYLIIFFMGVLGNGLSIYV--LQPYKSTSVN 74

DB 1 MEHNSFRVDS-----EFRYTLFPIYVSVIFILGVANGVYLVWVANLPYPSKLLNBIK 53
 QY 75 VFMNLALISDLLEISTLPFRADYLRKSNWIFGDLACRIMSYLSIYVNTSSIFYELTVLSV 134
 DB 54 IFMVLMTADLLEITLPLMIYIYNEGMILPNFLCNVAGCLFPIINTYCSVAFGLVITY 113
 QY 135 VRFPLAVNHPRLHNTSISAWILGIIIMILMASSIMLDSGS-----RONGSVTSC 187
 DB 114 NKQAVAVYIKRQATTRKRGISLSIIIVSIVATASVTLADSTNVLNKNKSGNITTC 173
 QY 188 LB-LNLKYIAKLQTMNYALVVG--LLEPFTLSICYLLIIRVLKVEVPSGLRVSHRA 245
 DB 174 FPHYEVSVPIIVNVHFIAF---CFELVFFLIFPCNLVLIHTLLIQPMKQRRKAGVKRA 230
 QY 246 LTTIIITLIFELCPPLRYHTLRVHLTTWKVGLCKDRILHKL-----VTLALAAANACPN 301
 DB 231 LMMVCTVLAFLICVPHHVQ--LPMTLAEIay-QTNFQALINDAQITLLCLSTNCVID 288
 QY 302 PLIYFAGENFDRRLKSAALRKGHPQAKTKC 332
 DB 289 PVIYCFELTKKFRKHS---EKFSMRSSRKC 316

RESULT 14

565518
 proteinase-activated receptor 2 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S65518; S64709; G02131
 R:Vysedc, S.; Emlisson, K.; Larsson, A.K.; Strombeck, B.; Sundelin, J.
 Eur. J. Biochem. 232, 84-89, 1995
 A:Title: Molecular cloning and functional expression of the gene encoding the human prote
 A:Reference number: S65518; MUID:96048032; PMID:7556175
 A:Accession: S65518
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-397 <NVS>

A:Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:G1008084; PIDN:CAA90290.1; PID:G1008
 R:Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn,
 Biochem. J. 314, 1009-1016, 1996
 A:Title: Molecular cloning, expression and potential functions of the human proteinase-ac
 A:Reference number: S64709; MUID:96177879; PMID:8615752
 A:Accession: S64709
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-137, A', 139-397 <BOE>
 A:Cross-references: EMBL:U34038; NID:G1041728; PIDN:AA847871.1; PID:G1041729
 R:Kahn, M.L.; Coughlin, S.R.
 submitted to the EMBL Data Library, September 1995
 A:Reference number: H00822
 A:Accession: G02131
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 29-397 <KAH>
 A:Cross-references: EMBL:U36753; NID:G1208539; PIDN:AAA90957.1; PID:G1208540
 C:Genetics:
 A:Map position: 5q13
 A:Introns: 28/1
 C:Superfamily: ATP receptor P2u
 F:1-36/Domains: activation peptide #status predicted <APR>
 F:1-25/Domains: signal sequence #status predicted <SIG>
 F:37-397/Product: proteinase-activated receptor 2 #status predicted <MAT>

Query Match 22.4%; Score 400.5; DB 2; Length 397;
 Best Local Similarity 30.7%; Pred. No. 3.1e-25;
 Matches 99; Conservative 69; Mismatches 121; Indels 33; Gaps 9;

QY 40 FPPYIYLIIFMGVLGNGLSIYVFLQPYKSTSVNVFNLALISDLLEISTLPFRADYTL 99
 DB 77 FLPIYIYIVFVGGVPSNMAWVFLFRYKKGKPAVYANALADLSVIFPLKIVYHI 136
 QY 100 RGSNMIFEDDLACRIMSYLSIYVNTSSIFYELTVLSVFRPLAVNHPRLHNTSISAWILC 159

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Db      137 HGNMNYGALCNVLIGFPGNMYSILEMTCLSVGRWYIVNPMG-----SRKANTAI 192
Qy      160 GI---IWIIMASSIML-----IDSGSEONGSVTSCLEMLYKIAKLQTMNY-I 204
Db      193 GISLAIMWLLILVTLFPLVVKQTFIPAL-----NITTCHEVLPBQLVGDMEFYPL 244
Qy      205 ALVGC-LLPFTLSICYLIIIRVLLKAVPESGLRVSHRKALTTIIITLIIIFLCFLPY 263
Db      245 SLAIGVFLFPAFLTASAVYVLMIRLSSAMDENSEK-KRRRAIKLIVTLVAMYLICETPS 303
Qy      264 HTLRFTVHLTVMYGLCKDRHLKALVTTLAAANACFNPFLVYFAGENFKORLKSALRK 323
Db      304 NLLLVHYFLIK-SQGSHVYALYIYALCLSTLNSCIDPEFYIFVSHDRHAKNALL-- 360
Qy      324 HQKAKTKCVPFVSVMLEKTR 345
Db      361 -CRSVRTVVKQMOVSLTSKHSR 381

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RESULT 15

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138435
angiotensin receptor homolog APJ - human
C/Species: Homo sapiens (man)
C/Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C/Accession: I38435
R/O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr
Gene 136, 355-360, 1993
A/Title: A human gene that shows identity with the gene encoding the angiotensin recepto
A/Reference number: I38435, MUID:94124031, PMID:8294032
A/Accession: I38435
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-380 <RES>
A/Cross-references: UNIPROT:P35414; EMBL:U03642; NID:9425351; PIDN:AAA18954.1; PID:94253
C/Genetics:
A/Map position: 11q12
A/Introns: #status absent
A/Superfamily: vertebrate rhodopsin

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Query Match      22.3%; Score 398; DB 2; Length 380;
Best Local Similarity 29.2%; Pred.No.4.7e-25;
Matches 100; Conservative 71; Mismatches 134; Indels 38; Gaps 13;

Qy      17 MEPNGTFSN-----NNSRNCTIENFKRE--FPPIVLIIFFWGVLGNGLSIY-VFLQPYKK 69
Db      1 MREGDQFDNYGADNGSECEYTDKSSGALIPAIYMLVFLGTGNGLVLMVTFRSRREK 60

Qy      70 STSVNVEMLNLAIIDLFTSTLPFRADYYLRGSNMIFGDLACRIMSYSLYVNNYSSIVFL 129
Db      61 RRSADIFIASLAVADLTFTVTLPLMATYTRDYDMPFGTFPCLSYLIFFVMYASVFCI 120

Qy      130 TILSVVRPLAMHPRPLLVHTSIRSAMILCGIIML--IMASSIML-DSGSEONGSVTS 186
Db      121 TGISFDRIYAIRVPAVNAARLRVSGAVATPAVLMAIALAMPVMLRTTGDLNNTKVO 180

Qy      187 CLELNLYKIAKLQTM-----NMYIALVVGCLLPFTLSICYLIIIRVLL-----KVEY 233
Db      181 CY-MDSYMAVATVSEWAMEVGLSVSTYGVFVPTIMLTCTFYIAQTIAGHRKERIF- 238

Qy      234 PRSGLRVSHRKALTTIIITLIIIFLCFLPYHLRTVH---LTTWKVGLCKDRHLKALVI 289
Db      239 ---GLR-KRRRLISIVLVVTFALCMMPYHLVKTLYMLGSLHMP---CDFDLPLMNIF 291

Qy      290 --TLAALAAACFNPFLVYFAGENFKORLKSALRKHPQAKT 330
Db      292 PYCTCISYVNSCLNPLVAFPDPRFOACTSMGCCGSRCAGT 334

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Search completed: March 18, 2005, 16:21:23
 Job time : 28.1272 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 20:14:54 ; Search time 205.232 Seconds
(without alignments)
8259.718 Million cell updates/sec

Title: US-09-826-791A-5

Perfect score: 1041

Sequence: 1 atgagagaaataatcgtc.....gaaggaacaagactataa 1041

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202764 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1037.8	99.7	1401	US-09-585-876-1	Sequence 1, Appl
2	145.2	13.9	1578	US-09-044-404A-1	Sequence 1, Appl
3	145.2	13.9	1578	US-09-586-924-1	Sequence 1, Appl
4	99.4	9.5	1020	US-09-170-496D-31	Sequence 31, Appl
5	99.4	9.5	1901	US-09-016-434-1484	Sequence 1484, Ap
6	99.4	9.5	1901	US-08-153-848-43	Sequence 43, Appl
7	99.4	9.5	1901	US-09-299-843A-43	Sequence 43, Appl
8	99.4	9.5	1901	US-09-088-337B-43	Sequence 43, Appl
9	99.4	9.5	1901	PCT-US93-11153-43	Sequence 43, Appl
10	99.4	9.5	2453	PCT-US95-07180-1	Sequence 1, Appl
11	96.2	9.2	1020	US-09-170-496D-181	Sequence 181, App
12	92	8.8	1255	US-08-097-938-3	Sequence 3, Appl
13	92	8.8	1255	US-08-476-000-3	Sequence 3, Appl
14	92	8.8	1255	US-08-476-840-3	Sequence 3, Appl
15	92	8.8	1255	US-08-476-976-3	Sequence 3, Appl
16	92	8.8	1255	US-08-474-410-3	Sequence 3, Appl
17	92	8.8	1255	US-08-486-673B-3	Sequence 3, Appl
18	90	8.6	1224	US-08-742-440A-1	Sequence 1, Appl
19	90	8.6	1414	US-08-476-000-62	Sequence 62, Appl
20	90	8.6	1414	US-08-472-840-62	Sequence 62, Appl
21	90	8.6	1414	US-08-476-976-62	Sequence 62, Appl
22	90	8.6	1414	US-08-474-410-62	Sequence 62, Appl
23	90	8.6	1414	US-08-486-673B-62	Sequence 62, Appl
24	85.6	8.2	1567	US-08-889-108-16	Sequence 16, Appl
25	85.6	8.2	1567	PCT-US94-10358-16	Sequence 16, Appl
26	85.6	8.2	2706	US-08-454-549-1	Sequence 1, Appl
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28	85.2	8.2	1452	1	US-08-149-093A-3	Sequence 3, Appl
29	85.2	8.2	1452	1	US-08-911-245-3	Sequence 3, Appl
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31	85.2	8.2	1452	2	US-08-514-451A-3	Sequence 3, Appl
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33	85.2	8.2	1452	3	US-09-510-473-3	Sequence 3, Appl
34	85.2	8.2	1452	3	US-09-048-916B-3	Sequence 3, Appl
35	84.4	8.1	1551	4	US-09-016-434-1239	Sequence 1239, Ap
36	84.4	8.1	1551	4	US-09-023-655-1186	Sequence 1186, Ap
37	84.4	8.1	1780	4	US-09-034-272-1	Sequence 1, Appl
38	83.2	8.0	1098	4	US-09-170-496D-225	Sequence 225, App
39	82.4	7.9	2706	3	US-08-676-351-1	Sequence 1, Appl
40	81.6	7.8	1098	4	US-09-170-496D-117	Sequence 117, App
41	81.6	7.8	1597	2	US-08-724-974A-1	Sequence 1, Appl
42	81.6	7.8	1597	4	US-09-364-425B-26	Sequence 26, Appl
43	81.4	7.8	1164	4	US-09-170-496D-107	Sequence 107, App
44	81.4	7.8	1164	4	US-09-170-496D-221	Sequence 221, App
45	81.4	7.8	2051	4	US-09-016-434-1259	Sequence 1259, Ap

ALIGNMENTS

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RESULT 1
US-09-585-876-1
; Sequence 1, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Siles-Santiago, Immaculada
; TITLE OF INVENTION: 43239, A No. 6586205el GPCR-like Molecule and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 5800-88
; CURRENT APPLICATION NUMBER: US/09/565, 876
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: 60/182,061
; EARLIER FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197) ... (1237)
US-09-585-876-1
Query Match 99.7%; Score 1037.8; DB 4; Length 1401;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1039; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 ATGAGAGAAATTTATGTCCTTGCACACCATCATCTCCGTATCAGAAATGAAACCAAT 60
197 ATGAGAGAAATTTATGTCCTTGCACACCATCATCTCCGTATCAGAAATGAAACCAAT 256
61 GGCACCTTCAGCAATPAACAACGACGAACTGCACATTTGAAACTTCAAGAGAGATTT 120
257 GGCACCTTCAGCAATPAACAACGACGAACTGCACATTTGAAACTTCAAGAGAGATTT 316
121 TTCCCAATTTGATATCTGATATATTTTCTGCGGAGCTTGGGAAATGGGTTTCATTA 180
317 TTCCCAATTTGATATCTGATATATTTTCTGCGGAGCTTGGGAAATGGGTTTCATTA 376
181 TATGTTTCTGACAGCTTATPAAGATCCATCTGTGAAGCTTTTCATGCTTAATCTG 240
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437 GCATTTAGATCTCTGTTTCATPAAGACGCTTCCCTTCAGGCGCTGACTTATATCTTGA 496
301 GGCTCCATTTGATTTTGGAGACCTGGCGCTGCAGAGATTATGCTTATTTCTTGTATGTC 360
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QY	481	ATCATATGAGATCCTTATCATGAGCTTCCCTCAATTAATGCTCCTGACAGTGGCTTGAGCAG	540
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QY	541	AACGGCAGTGCACATCATGTCTTAGAGCTGAATCTCTTAAATTTGCTAAGCTGCAGACC	600
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QY	601	ATGAACATATATGCGCTGTGTGGTGGGCGCCGCTGCGCATTTTTCACACTGACAGATCTGT	660
Db	797	ATGAACATATATGCGCTGTGTGGTGGGCGCCGCTGCGCATTTTTCACACTGACAGATCTGT	856
QY	661	TATCTGCTGATCATTCGGGTTCTGTAAAGGTGAGAGTCCAGAAATCGGGGCTGGGGTT	720
Db	857	TATCTGCTGATCATTCGGGTTCTGTAAAGGTGAGAGTCCAGAAATCGGGGCTGGGGTT	916
QY	721	TCTCACAGGAAGGCACTGACCAACCATCATCATCACTTGATCATTTCTTCTGTGTGTTTC	780
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QY	781	CTGCCCTATCACACACTGAGACCGTCCACTGTGACGACATGAGAAAGTGGGTTTATGCAAA	840
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QY	841	GACAGACTGCATAAAGCTTTGGTTATCATCACTGCGCTTGGACAGACCAATGCTGCTTC	900
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QY	901	AATCTCTGCTCTATTAATCTTTGCTGGGGGGAATTTTAAGACAGACTAAAGCTGACATC	960
Db	1097	AATCTCTGCTCTATTAATCTTTGCTGGGGGGAATTTTAAGACAGACTAAAGCTGACATC	1156
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QY	1021	AGAAAGGAAACAAGATATA 1041	
Db	1217	AGAAAGGAAACAAGATATA 1237	

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1      RESULT 2
2      US-09-044-404A-1
3      Sequence 1, Application US/09044404A
4      Patent No. 6200775
5      GENERAL INFORMATION:
6      APPLICANT: SATHE, GANESH
7      APPLICANT: SATHE, WENDY
8      APPLICANT: HALSEY, WENDY
9      APPLICANT: ELLIS, CATHERINE
10     APPLICANT: AMES, ROBERT
11     APPLICANT: FOLEY, JAMES
12     APPLICANT: SARAI, HENRI
13     TITLE OF INVENTION: CDNA CLONE HMTMB1 THAT ENCODES
14     TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
15     NUMBER OF SEQUENCES: 2
16     CORRESPONDENCE ADDRESS:
17     ADDRESSEE: SmithKline Beecham Corporation
18     STREET: 790 Swedeland Road, P.O. Box 1539
19     CITY: King of Prussia
20     STATE: PA
21     COUNTRY: USA
22     ZIP: 19406

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1 COMPUTER READABLE FORM:
2
3 MEDIUM TYPE: Diskette
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5 COMPUTER: IBM Compatible
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7 OPERATING SYSTEM: DOS
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9 SOFTWARE: FastSeq for Windows Version 2.0
10
11 CURRENT APPLICATION DATA:
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13 APPLICATION NUMBER: US/09/044,404A
14
15 FILING DATE: MARCH 19, 1998
16
17 CLASSIFICATION: 435
18
19 PRIOR APPLICATION DATA:
20
21 APPLICATION NUMBER: 08/844,795
22
23 FILING DATE: APRIL 22, 1997
24
25 ATTORNEY/AGENT INFORMATION:
26
27 NAME: Han, William T.
28
29 REGISTRATION NUMBER: 34,344
30
31 REFERENCE/DOCKET NUMBER: GH-70001-1
32
33 TELECOMMUNICATION INFORMATION:
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35 TELEPHONE: 610-270-5219
36
37 TELEFAX: 610-270-5090
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39 TELEX:
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41 INFORMATION FOR SEQ ID NO: 1:
42
43 SEQUENCE CHARACTERISTICS:
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45 LENGTH: 1578 base pairs
46
47 TYPE: nucleic acid
48
49 STRANDEDNESS: single
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51 TOPOLOGY: linear
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53 MOLECULE TYPE: cDNA
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Query Match	13.9%	Score 145.2	DB 3	Length 1578
Best Local Similarity	51.5%	Pred. No. 1.6e-35		
Matches 451	Conservative 0	Mismatch 358	Indels 27	Gaps 4
QY	93	CACAAATGAAACCTTCAAGAGAGAAATTTTCCCAATGTATATCTGATTAATATTTTCTG	152	
Db	514	CACATATTAGAGACTTCGGCAATCAAGGTATATTCACCTTGACTATAGATCTCTGTGT	573	
QY	153	GGGAGTCTTGGGAATGGGTTCACATATATGTCTTGAGGCTTATGAAGTCCAC	212	
Db	574	AGGGTTCTTGGCAATGGCTTTGTGCTCTATGTCTATATAAACCTATCAAGAAAGTC	633	
QY	213	ATCTGTAAAGTTCATNGCTAAATCTGGCCATTTAGATCTCCGTTCATAAACACGCT	272	
Db	634	AGCCTTCCAAGTATACATGATTAATTAGACATGACAGATCTACTTTGTGTGACACT	693	
QY	273	TCCCTCAGGCGTACATTAATCTTAAAGGCTCCATTTGATATTGGAGACTGGCCTG	332	
Db	694	GCCTCTCCGTGTGATTAATGTCCAAAAGGCAATTTGGCTCTTGGTGACTTCTGTG	753	
QY	333	CAGATTAATCTTATCTCTTGATATGCAACATGACAGAGATTTATTCCTGACCGT	392	
Db	754	CCGCTCAGACCTTATGCTTTGATGTCAACTTATATGACATCTTCTTAATGACAGC	813	
QY	393	GCTGAGTGTGTGCGTTCCCTGGCAAGTTCACCCCTTGGCTTCGACTGCACGAG	452	
Db	814	CATGAGCTTTTCCGGTGACATGGAATGTCTTTCCAGTCAGAAACATTAATTTGGTTAC	873	
QY	453	CATCAGAGTGCCTGATCTCTGTGGGATCATATGATCTT--ATCATGGCTTCTC	509	
Db	874	ACAGAAAAAGCCAGGTTGTGTGTGATGAGTATTTGGATTTTGTGATTTTGACCAAGTTC	933	
QY	510	AATTAATCTCTGGACAGTGGCTCTGAGCAAGACGAGTGTCAATCATGCTTAGAGCT	569	
Db	934	TCCATTTCTATGGCCAAACCAAAABAGATGGGAAAAATATATCCAAAGTCTTTGAGCC	993	
QY	570	GAATCTCTATAAATGCTAAGTGCA-----GACCATGAACATTAATGCGTTGGTGT	623	
Db	994	CCCAACAAGACATCAACCTAAATCATGTTTGGTCTTGATATATGTCATTTGTTGT	1053	
QY	624	GGGCTGCTGCTGCATTTTTCACATCAGACATCTGTATCTGCTGATCATTCGGGTCT	683	
Db	1054	TGGCTTATATATCCCTTTGTATTAATAATGTCTGTGTAACAAATGATCAATTTTGACCTT	1113	

QY 684 GTTAAAGTGAAGTCCAGAAATCGGGGCTGGGGTTCTCAGAGAGCACTGACAC 743
| | | | |
DB 1114 ACTAABAAAATCAATCAAAAATCTGTCAG-----TCATAAAAGCTATAGAAAT 1167
| | | | |
QY 744 CATCATCATACCTTGATCATCTCTCTGTTGTTCTGCCCCATCACAACCTGAGAC 803
| | | | |
DB 1168 GATCATGTCGTGACCGCTGCTGCTTTTATGTCAGTTTCATGCAATCATATTCAGAGTAC 1227
| | | | |
QY 804 CGTCCACTT-----GACGACATGAAAGGGTTATGCAAGACAGACTGCA 851
| | | | |
DB 1228 CATTCACCTTCATTTTTCACAAATGAACTAAACCTTGATCTGTCTTGAATGCA 1287
| | | | |
QY 852 TAAAGCTGTTGTTATCAGACTGAGCTTGAGCAGCAATGCTGCTTCAATCTCTGCT 911
| | | | |
DB 1288 GAAGTCCTGTCATTAACCTTGTCTGCTGCTGATCAATTTGTTGCTTGAACCTCTCT 1347
| | | | |
QY 912 CTATTACTTTGCTGGGAGAAATTTTAAAGACAGACT 947
| | | | |
DB 1348 ATATTCTTTCTGGGGGTAACTTTAGAAAAGGCT 1383
| | | | |

RESULT 3
US-09-586-924-1
; Sequence 1, Application US/09586924
; Patent No. 6506878
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH M.
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: AMES, ROBERT S.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: CHAMBERS, JON
; TITLE OF INVENTION: CDNA CLONE HMTMP81 THAT ENCODES A NOVEL
; FILE REFERENCE: GH-70001-1D1
; CURRENT APPLICATION NUMBER: US/09/586,924
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 09/044,404
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/844,795
; PRIOR FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-586-924-1

Query Match 13.9%; Score 145.2; DB 4; Length 1578;
Best Local Similarity 51.5%; Pred. No. 1.6e-35;
Matches 451; Conservative 0; Mismatches 398; Indels 27; Gaps 4;
QY 93 CACAATGAAACTTCAAGAGAAATTTTCCCAATTTGATATCTGATATAATTTTCTG 152
| | | | |
DB 514 CACTATTTGATGACTTCGGCAATCAAGTGAATTCACCTTGATCTATGATCTCTGTGT 573
| | | | |
QY 153 GGGAGCTTGGGAAATGGGTTGTCATATATGTTTCTGACAGCTTATAGAAAGTCCAC 212
| | | | |
DB 574 AGGCTTCTTGGCAATGGCTTTGTGCTCTATGTCCTCATATAAACTATCAAGAAAGTC 633
| | | | |
QY 213 ATCTGTGAACGTTTCATGCTAAATCTGGCAATTCAGATCTCTGTTCATAAGACGCT 272
| | | | |
DB 634 AGGCTTCAAGTATACATGATTAATTTAGAGTAGAGATCTACTTTGTGTGACACACT 693
| | | | |
QY 273 TCCCTTCAAGGCTGATATATCTTAGAGGCTCAATGATTTTGAGAACTGGGCTG 332
| | | | |
DB 694 GCTCTCCGTGTGCTTATATATGCCAAGGCAATTTGGCTTTGGTACTTTCTTG 753
| | | | |
QY 333 CAGAGTATATCTTATCTTGTATGCAACATGATGACAGATTAATTTCTGACCGT 392
| | | | |
DB 754 CGGCTCAGACCTATGCTTTGTATGCAACCTCTATGATGACATCTTCTTATGACAGC 813
| | | | |

QY 393 GCTGAGTGTGTGCGCTTCTCGGCAATGCTTCAACCCCTTTCGGCTTCTGATGCAACAG 452
| | | | |
DB 814 CATGAGCTTTTCCGGTGATGCAATTTGTTTCCAGTCCAGAACATTAATTTGGTTAC 873
| | | | |
QY 453 CATCAGAGTGTGCTGATCTCTGTGGGATCATATGATCTCT--ATCATGGCTTCTTC 509
| | | | |
DB 874 ACAGAAAAAGCAGGTTGTGTGTAGAGTATTTGATTTTGTGATTTTGAACCAAGTTC 933
| | | | |
QY 510 AATATGCTCTCGAGACAGTGGCTGTGAGAGAAACGCACTGTCAATCATGCTTGAAGCT 569
| | | | |
DB 934 TCCATTTCTTAATGGCCAAACCAAAAAGATGGAAAAATTAATCCAGTCTTGAGGC 993
| | | | |
QY 570 GAATCTTATAAATTTGCTTAACTGCA-----GACATGAATATATATGCTTGGTGT 623
| | | | |
DB 994 CCCAAGACATTCAAATCTAAATATATGTTTGGCTTGCATATATGTCATTTGTTGT 1053
| | | | |
QY 624 GGGCTGCTGCTGCAATTTTTCACACTGACATCTGTATCTGCTGATCATTTGGGTTCT 683
| | | | |
DB 1054 TGGCTTATCATCCCTTTGTTATATATGTGCTGTTACAAATGATCATTTTGAACCTT 1113
| | | | |
QY 684 GTTAAAGTGAAGTCCAGAAATCGGGGCTGGGGTTTTCACAGAAAGCACTGACAC 743
| | | | |
DB 1114 ACTAABAAAATCAATCAAAAATCTGTCAG-----TCATAAAAGCTATAGAAAT 1167
| | | | |
QY 744 CATCATCATACCTTGATCATCTCTCTGTTGTTCTGCCCCATCACAACCTGAGAC 803
| | | | |
DB 1168 GATCATGTCGTGACCGCTGCTGCTTTTATGTCAGTTTCATGCAATCATATTCAGAGTAC 1227
| | | | |
QY 804 CGTCCACTT-----GACGACATGAAAGGGTTATGCAAGACAGACTGCA 851
| | | | |
DB 1228 CATTCACCTTCATTTTTCACAAATGAACTAAACCTTGATCTGTCTTGAATGCA 1287
| | | | |
QY 852 TAAAGCTGTTGTTATCAGACTGAGCTTGAGCAGCAATGCTGCTTCAATCTCTGCT 911
| | | | |
DB 1288 GAAGTCCTGTCATTAACCTTGTCTGCTGCTGATCAATTTGTTGCTTGAACCTCTCT 1347
| | | | |
QY 912 CTATTACTTTGCTGGGAGAAATTTTAAAGACAGACT 947
| | | | |
DB 1348 ATATTCTTTCTGGGGGTAACTTTAGAAAAGGCT 1383
| | | | |

RESULT 4
US-09-170-496D-31
; Sequence 31, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-31

Query Match 9.5%; Score 99.4; DB 4; Length 1020;
Best Local Similarity 48.8%; Pred. No. 5.3e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;
QY 119 TTTTCCCAATTTGATATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGTTGTCCA 178
| | | | |
DB 98 TGTTCGCTCCCTTCAACCTTGTGATTTATCTGGCTTTAGTTGCAATACCTGAGCTC 157
| | | | |
QY 179 TATATGTTTCTGACGCTTATTAAGAGTCCACATCTGTGAACGTTTTCATGCTAAATC 238
| | | | |

158 TGTGCTTTTCATCCGAGACCAAGTCGGAGACCCCGGCAACGTTCTTGATGATC 217
QY 239 TGGCATTTCAGATTCCTGTTATAGACAGCTTCCCTTCAAGGCTGATATATCTTA 298
Db 218 TGGCCGTGGCCGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 277
QY 299 GAGGCTCCATATGATATTTGAGACCTGGCTGACAGATTAATGATCTTAATCTTGTANG 358
Db 278 CTGGGAACCACTGGCCATTTGGGGAATGCAATCCGCTCAACCGGCTTCTTCTTACC 337
QY 359 TCAACATGTAACAGACGATATTTATTTCTTGAACGCTGCTGAGTGTGCTTCTGCA 418
Db 338 TCAACATGTAACGCAACATCTACTTCTCACTGCACTGACGCGGCAACCTGCTTCTG 397
QY 419 TGGTTACCCCTTGGCTTGTGCAATGTAACGACGACGAGAGTGGCTGATCTCTGTG 478
Db 398 TGTGTGACCCCGTCAAGTCCCTCAAGCTCCGACGCGCCCTTCAACGACACCTGGCTGTG 457
QY 479 GGATCATATGATCTTATCATGCTTCTTCAATTAATGCTCTGGAAGTGGCTTGAGC 538
Db 458 CCTTCTGTGGT 517
QY 539 AGAACGGAGTGTACATCATGCTTGAAGCTGAATCTATAAATTTGCTTAAGCTGACAG 598
Db 518 TGAAGACCAACCAACGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 577
QY 599 CCATGACATATATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 658
Db 578 CCTGTG-----TGTCCCTGGAGTGGCCCTTCACTCCGTTCACTACACACGCTGACT 631
QY 659 GTTATGTGCTGATCATTCGGGTTCTGTAAAGTGAAGTCCCAATGCGGCGCTGCGG 718
Db 632 GCTACTGTGTGATCATCCGACGCTCGGACGCGCTGCTGTGTGTGTGTGTGTGTGTGT 690
QY 719 TTTCTCAAGAGAGGACGTGACCAACCATCATCATCTTGATCATCTTCTTGTGTGT 778
Db 691 -----ACCAAGGAGTGGCGCATGATGCGCATGTGCGGCATCTTCTGTGTGTGT 742
QY 779 TCTGTGCTTATCAGACATGAGGACCGTCACTTG 813
Db 743 TGTGTGCTTACCACTGCAACCGCTCGCTGTACGTG 777

RESULT 5
US-09-016-434-1484
; Sequence 1484, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1484:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 992699
; US-09-016-434-1484

Query Match 9.5%; Score 99.4; DB 4; Length 1900;
Best Local Similarity 48.8%; Pred. No. 86-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

QY 119 TTTTCCCATTTGTATATCTGATTAATATTTTCTGAGGAGCTTGGGAATGGGTTGTCCA 178
Db 797 TGTGCGCTCTTCTACTCTTGATTTTATCTGAGCTTATGAGCAATACCTGGCTC 856
QY 179 TATATGTTTCTGAGCTTATTAAGAGTCCACATCTGTGAACGTTTTCATCTTAATC 238
Db 857 TGTGCTTTTCATCCGAGACCAAGTCCGGAGCCCGGACAGGTTCGTAAGCATC 916
QY 239 TGGCATTTCAGATCTCTGTTTATAGACACGCTTCCCTTCAAGGCTGACTTATCTTA 298
Db 917 TGGCGGTGGCCGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 976
QY 299 GAGGCTCAATGATATTTTGAAGACTGAGCTGAGAGATTATGCTTATCTTGTATG 358
Db 977 CTGGGAACCACTGGCCATTTGGGAAATGCAATGCGCTTCAACCGGCTTCTTCTTACC 1036
QY 359 TCAACATGTAACGAGATTTTATTTCTGACCGGTGTAGTGTGTGTGTGTGTGTGTGT 418
Db 1037 TCAACATGTAACGAGATTTTATTTCTGACCGGTGTAGTGTGTGTGTGTGTGTGTGT 1096
QY 419 TGTTCACCCCTTGTGGCTTGTGACATGTCACGAGATGAGAGTCCGTGATCTCTGTG 478
Db 1097 TGTGTGACCCGCTCAAGTCCCTCAAGCTCCGAGGCGCTTCAACGACACCTGGCTGTG 1156
QY 479 GGATCATATGATCTTATCATGCTTCTCTAATATGCTCTGACAGTGGCTGTGAGC 538
Db 1157 CCTTCTGTGGT 1216
QY 539 AGAACGGAGTGTACATCATGCTTGAAGCTGAATCTATATAATTTGTAAGCTGACAG 598
Db 1217 TGAACACCAACCAACGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1276
QY 599 CCATGACATATATGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 658
Db 1277 CCTGTG-----TGTCCCTGGAGTGGCTTACTTCCGTTCACTACACAGGTCACT 1330
QY 659 GTTATGTGCTGATCATTCGGGTTCTGTTAAAGTGAAGTCCCAAGATCGGGGCTGCGG 718
Db 1331 GCTACTGTGTATCATCCGACGCTCGGACGAGGCTGTGTGTGAAGAGCGCTCAAG- 1389
QY 719 TTTCTCAAGAGAGCACTGACCAACATCATCATCTTGATCATCTTCTTCTTGTGT 778
Db 1390 -----ACCAAGGACAGTGGCAATGATGCTGTGCTCATCTTCTGTGTGTGT 1441
QY 779 TCTGCGCTTATCAGACACTGAGGAGCGTCACTTG 813
Db 1442 TGTGTGCTTACCACTGCAACCGCTCGCTGTACGTG 1476

RESULT 6
US-08-153-848-43

Sequence 43, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 701..1717
US-08-153-848-43

Query Match 9.5%; Score 99.4; DB 1; Length 1901;
Best Local Similarity 48.8%; Pred. No. 8e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

QY 119 TTTTCCCAATGTAATCTGATTAATTTTTCGGGAGCTTGGGAAT3GGTGTGCA 178
DB 798 TGTTCGCCCTTCTTACCTTCTGATTTATCTGCTTAAGTGGCAATACCCTGCTC 857
QY 179 TATATGTTTCTGTGACCTTATAGAGTCCATCTGTGAACGTTTTCATGCTAAATC 238
DB 858 TGTGCTTTTCAATCCGAGACCAAGTCCGGGACCCGGCCAAACGTTTCGATGCATC 917
QY 239 TGGCCATTTCAATCTCCCTGTTTATAGAGACCGTTCCCTTACAGGCTGACTATATCTTA 298
DB 918 TGGCCGTGGCCGACCTTGT 977
QY 299 GAGGCTCCAAATGTAATTTTGGAGACCTGGCTGCAGATTAATGTTTATCTTGTATG 358
DB 978 CTGGGAACACATGCGCATTTGGGGAATATGCAATGCGCTCTCACCGGCTTCTTCTTACC 1037
QY 359 TCAACATGTACAGCACTATTTATTTCTCTGACCGTGTGAAGTGTGTGCGTTTCTGGCAA 418
DB 1038 TCAACATGTACAGCACTATTTCTCTGACCGTGTGAAGTGTGTGCGTTTCTGGCAA 1097
QY 419 TGGTTCAACCCCTTTGGGCTTCTGCAATGTACCAAGCATACAGAGTGTGCTGATCTCTGTG 478

DB 1098 TTGTGACCCCGGTCAAGTCCCTCAAGCTCCGAGGCCCCCTTACGACACACCTGGCTGTG 1157
QY 479 GGATCATATGATCTTATCATAGGCTTCTCTCAATATATGCTCTGACAGTGGCTTGAAC 538
DB 1158 CCTTCTGTGGGT 1217
QY 539 AAGACGGCAGTGTCAATCATATCTTAGAGCTGAATCTCTATATAATTTGTTAAGCTGACA 598
DB 1218 TCGAAGCAACCAACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1277
QY 599 CCATGAATATATTTGCTTGT 658
DB 1278 CCTGTG-----TGTCTCCGAGAGTGTGCTTACCTTCCGTTTATCATCACAGGTACCT 1331
QY 659 GTTATCTGTATCATTTGGGCTTCTGTATAAAGTAGAGTCCCAAGATGGGAGCTGCGAG 718
DB 1332 GCTACCTGTGTATCATCCGACAGCTGCGGACGGGCTGTGTGTGTGTGTGTGTGTGTGT 1390
QY 719 TTTCACAGGAAGGACCTGACCATCATCATCATCATCATCATCATCATCATCATCATCAT 778
DB 1391 -----ACCAAGCAGTGCAGCATGATCGCATATGTGTGTGTGTGTGTGTGTGTGT 1442
QY 779 TCCTGCCCTATCACACACTGAGAGCGTCCACTTG 813
DB 1443 TGTGTCTTACCACTGCAACGCTCGCTTACGTG 1477

RESULT 7
US-09-299-843A-43
Sequence 43, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: J111 E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 701..1717
US-09-299-843A-43

Query Match 9.5%; Score 99.4; DB 3; Length 1901;
Best Local Similarity 48.8%; Pred. No. 8e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

119 TTTTCCCAATGTAATCTGATAATATTTTCTGGGAGCTTGGGAATGGGTTGCA 178
798 TGTTCGCTCTCTTACCTTCTGATTTTATCTTGGCTTATGGCAATACCTGCTC 857
179 TATATGTTTCTGACAGCTTATTAAGATCCACATCTGNAACGTTTTCATGCTAATC 238
858 TGTGCTTTTATCCAGACCAAGTCCGGACCCCGCAAGGTTCCTGATGCATC 917
239 TGGCCATTTGAGATCTCTGTTCAATAGACAGCTTCCCTTCAGGCTGACTATTAATCTTA 298
918 TGGCCGTGGCGCACTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977
299 GAGGCTCCATTTGATATTTTGGAGACCTGGCTGCAAGATTAATGTTTCTTATGCTTGTATG 358
978 CTGGGAACCACTGCGCAATTTGGGAAATGCAATGCGCTCACCGGCTCTCTCTTACCC 1037
359 TCAACATGTAACAGATTAATTTCTGACCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 418
1038 TCAACATGTAACAGATTAATTTCTGACCTGCTGCAATGAGCGGACCGTTTCTGAGCA 1097
419 TGGTTACCCCTTTGGGCTTCTGATGTCAACAGATGAGAGTGGCTGATCTCTGTG 478
1098 TTGTGACCCGCTCAAGTCCCTCAAGTCCGAGGCGCTCAAGCAACCTGGCTGTG 1157
479 GATCATATGATATCTTATCATATGCTTCTGCAATTAATGCTCTGCAAGTGGCTGTGAGC 538
1158 CCTTCTGTGGGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1217
539 AGAAGCGAGTGCATCATATGCTTAGAGTGAATCTTATAAATTTGCTAAGCTGACA 598
1218 TGAAGACCAACCAAGGTGTGCTGCTGCACTGATCAGGAGAGGCTCCACCACTG 1277
599 CCATGATATATGCTTGT 658
1278 CCTGTG-----TGTCTGTGAGT 1331
659 GTTATGCTGATATCTGAGGTTCTGTAAAGTGAAGTCCCAAGATGGGGCTGCGG 718
1332 GCTACCTGTGATCATCCGAGCTGTGGCAGGGCTGTGCTGTGAGAAAGCCCTCAAG- 1390
719 TTTCTCAGAGAGGACTGACCAACCATCATATCACTTTGATCATCTTCTTGTGTT 778
1391 -----ACCAAGGAGTGGCATATGCCATATGCTGTGGCATCTTCTGTGTGCT 1442
779 TCTGCTCATATCAACACTGAGAGCGTCCACTTG 813
1443 TGTGTGCTTACCAAGTCAACCGCTCGTCTACGTG 1477

RESULT 8
US-09-088-337B-43
; Sequence 43, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Gray, Patrick W.
; Schweiakart, Vicki L.
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Born
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 701..1717
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-088-337B-43
Query Match 9.5%; Score 99.4; DB 3; Length 1901;
Best Local Similarity 48.8%; Pred. No. 8e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;
119 TTTTCCCAATGTAATCTGATAATATTTTCTGGGAGCTTGGGAATGGGTTGCA 178
798 TGTTCGCTCTCTTACCTTCTGATTTTATCTTGGCTTATGGCAATACCTGCTC 857
179 TATATGTTTCTGACAGCTTATTAAGATCCACATCTGNAACGTTTTCATGCTAATC 238
858 TGTGCTTTTATCCAGACCAAGTCCGGACCCCGCAAGGTTCCTGATGCATC 917
239 TGGCCATTTGAGATCTCTGTTCAATAGACAGCTTCCCTTGAAGGCTGACTATTAATCTTA 298
918 TGGCCGTGGCGCACTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 977
299 GAGGCTCCATTTGATATTTTGGAGACCTGGCTGCAAGATTAATGCTTATGCTTGTATG 358
978 CTGGGAACCACTGCGCAATTTGGGAAATGCAATGCGCTCACCGGCTTCTTCTTACC 1037
359 TCAACATGTAACAGATTAATTTTCTGACCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 418
1038 TCAACATGTAACAGATTAATTTCTGACCTGCTGCAATGAGCGGACCGTTTCTGAGCA 1097
419 TGGTTACCCCTTTGGGCTTCTGATGTCAACAGATGAGAGTGGCTGATCTCTGTG 478
1098 TTGTGACCCGCTCAAGTCCCTCAAGTCCGAGGCGCTCTTACGACACCTGAGCTGTG 1157
479 GATCATATGATCTTATCATATGCTTCTGCAATTAATGCTCTGGAACAGTGGCTGTAGC 538

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Db      1158 CCTTCTGTGGGTGGTGGTGGTGGCCATGAGCCCCGCTGCTGGAGACCCACAGACCG 1217
Qy      539 AGAAGCGAGGTGTACATCATCTAGACCTGAATCTTAATAATTGCTTAAGTCGAGA 598
Db      1218 TGCAGACCAACCAACGAGTGTGCTGCTGACGTGAACGGAGAGGCTCCACACATG 1277
Qy      599 CCATGAACATATATTCCTGTGTGGTGGGCTGCTGTCATTTTCAACTCAGATCT 658
Db      1278 CCTGG-----TGTCCCTGGAGTGGCCCTTCACCTCCGTTCAACACGCTACCT 1331
Qy      659 GTTATCTGTGATCATCTGGGTTCTGTAAAGTGAAGTCCAGAAATCGAGCTGCGGG 718
Db      1332 GCTACCTGTGATCATCCGACGCTGCGGAGGCGCTGCTGTGAGAAAGTCCCTCAAG- 1390
Qy      719 TTCTCAAGAGGAGCTGACCAACCATCATCATCACTTGAATCTTCTTGTGT 778
Db      1391 -----ACCAAGGAGAGTGCATATGCAATAGTGTGGCAATCTTCTGTGCT 1442
Qy      779 TCTGCCCCATGACACACTGAGAGACCGTCCACTTG 813
Db      1443 TGTGCCCCAACAAGTCAACCGCTCCGTCTACGTG 1477

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RESULT 9

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PCT-US93-1153-43
/ Sequence 43, Application PC/TUS9311153
/ GENERAL INFORMATION:
/ APPLICANT: Godiska, Ronald
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: Schwellhart, Vicki L.
/ TITLE OF INVENTION: Novel Seven Transmembrane Receptors
/ NUMBER OF SEQUENCES: 64
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ ADDRESSEE: Bicknell
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/11153
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/977,452
/ FILING DATE: 17-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Noland, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 31794
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1901 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 701..1717
/ PCT-US93-1153-43

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Query Match 9.5%; Score 99.4; DB 5; Length 1901;
 Best Local Similarity 48.8%; Pred. No. 86-21;
 Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;

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Qy      119 TTTTCCCAATTGATATATCTGATATATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCA 178
Db      798 TGTTCGCCCTCTTCAACCTTCTGATATTTATCTGGCTTTAGTTGGCAATACCTGTGCTC 857
Qy      179 TATATGTTTCTGTGACCTTATTAAGAACTCCACATCTGTGAACGTTTCAATGCTAATTC 238
Db      858 TGTGGCTTTTCAATCCGAGACCAAGTCCGGAGACCCCGGCAACGTTTCTGATGCAATC 917
Qy      239 TGGCCATTTCAATGTCCTGTTTATTAAGACAGCTTCCCTTGAGGGGTGACTAATTAATCTTA 298
Db      918 TGGCCGTGGCCGACTTGTGTGCTGTGCTGTCTTGTCCACCGGCTGTGTACCACTTCT 977
Qy      299 GAGGCTCCAAATGATATTTGAGACCTGGGCTGAGAGATTAATGTTTATTCCTTGTATG 358
Db      978 CTGGGAACCACTGGGCATTTGGGGAATGCAATGCGGTCTACACGGGCTTCTCTTCTAC 1037
Qy      359 TCAACATGTACAGCATATTTATTTCTGACCGCTGTAGTGTGTGCGTTTCTTGGCAA 418
Db      1038 TCAACATGTACCGCAGCATCTTCTCTCACTGCAATGCGCGCAACCGTTTCTTGGCCA 1097
Qy      419 TGGTTACCCCTTTGGGCTTGTGCAATGTCACGAGATGACGAGTGCCTGATCCTGTG 478
Db      1098 TTGTGACCCGGTCAAGTCCCTCAAGCTCCGAGGCGCTTCAACGACACTGCGCTGTG 1157
Qy      479 GGATCATATGATACCTTATCATAGGCTTCTCAATATGCTCTCTGACAGTGGCTGTGAGC 538
Db      1158 CTTTCTGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1217
Qy      539 AGAAGCGAGGTGTACATCATCTTGAAGCTGAATCTTAATAATTGCTTAAGTCGAGA 598
Db      1218 TGCAGACCAACCAACGAGTGTGCTGCTGACCTGATGACCGGAGAGGCTCCACACATG 1277
Qy      599 CCATGAACATATATTCCTGTGTGGTGGGCTGCTGTCATTTTCAACTCAGATCT 658
Db      1278 CCTGG-----TGTCCCTGGAGTGGCCCTTACCTTCCGTTCAACACAGGTACCT 1331
Qy      659 GTTATCTGTGATCATCTGGGTTCTGTAAAGTGAAGTCCAGAAATCGAGCTGCGGG 718
Db      1332 GCTACCTGTGATCATCCGACGCTGCGGAGGCGCTGCTGTGAGAAAGCGCTCAAG- 1390
Qy      719 TTCTCAAGAGGAGCTGACCAACCATCATCATCACTTGAATCTTCTTGTGT 778
Db      1391 -----ACCAAGGAGAGTGCATATGCAATAGTGTGGCAATCTTCTGTGCT 1442
Qy      779 TCTGCCCCATGACACACTGAGAGACCGTCCACTTG 813
Db      1443 TGTGCCCCAACAAGTCAACCGCTCCGTCTACGTG 1477

```

RESULT 10

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PCT-US95-07180-1
/ Sequence 1, Application PC/TUS9507180
/ GENERAL INFORMATION:
/ APPLICANT: LI, YI
/ APPLICANT: GOCAYNE, JEANINE D
/ APPLICANT: RUBEN, STEVEN M
/ TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBBB69
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
/ ADDRESSER: STEWART & OLSTEIN
/ STREET: 6 BECKER FARM ROAD
/ CITY: ROSELAND
/ STATE: NJ
/ COUNTRY: US
/ ZIP: 07068
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2453 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 548..1564
PCT-US95-07180-1

Query Match 9.5%; Score 99.4; DB 5; Length 2453;
Best Local Similarity 48.8%; Pred. No. 9.5e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15; Gaps 2;
QY 119 TTTTCCCAATGTAATCTGATTAATTTTCTGGGAGTCTTGGGAATGGGTTGCCA 178
DB 645 TGTGCGCTCCTCTTACCTTCTGATTTATCCGCTTAGTTGGCAATACCTGGCTC 704
QY 179 TATATGTTTCTCGACGCTTAATAAGATCCACATCTGGAAGCTTTTAACTAAATC 238
DB 705 TGTGCTTTTATCCGAGACCAAGTCCGGACCCCGCAAGTGTCTTATGATC 764
QY 239 TGGGCAATTCAGATCTCTGTTCAATAGACGCTTCCCTTCAGGGCTGATTAATCTTA 298
DB 765 TGGCCGTGGCGGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 824
QY 299 GAGGCTCAATGGATATTTGAGACCTGCGCTGCAAGATTAATGTTCTTATCTTGTATG 358
DB 825 CTGGAAACACTGGCCATTTGGGAAATGCAATGCGTCTCACCGGCTTCTCTTACC 884
QY 359 TCAACATGTAACAGATTAATTTCTGACCGTGTGAGTGTGTCGCTTCTGACCA 418
DB 885 TCAACATGTAACAGATTAATTTCTGACCGTGTGAGTGTGTCGCTTCTGACCA 944
QY 419 TGGTTACCCCTTTCGCTTCTGATGTCAACGATCAAGAGTGCCTGATCTCTGTG 478
DB 945 TTGTGACCCCGGTCAAGTCCCTCAAGCTCGGAGCCCTCTACGACACTGGGCTGTG 1004
QY 479 GGAATCATATGATCTTATCATGATGCTTCTCAATATATGCTCTGACATGAGCTGTGAGC 538
DB 1005 CCTTCTGT 1064
QY 539 AGAAGCGAGTGTACATCATGCTTAAGCTGATCTTAATAATTTGTAAGCTGACA 598
DB 1065 TGCAGACCAACCAACGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1124
QY 599 CCATGAACATAATGCTGT 658
DB 1125 CCTGTG-----TGTCCCTGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1178
QY 659 GTTATCTGTGATCATTTGGGTTCTGTTAAAGTGAAGTCCAGAAATGGGGCTGGGG 718
DB 1179 GCTACCTGTGATCATCCCAAGCTTGGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGT 1237
QY 719 TTTTCTACAGAGGACATGACCAACATCATCATCACTTGTATCATCTTCTTGTGTGT 778
DB 1238 -----ACCAAGGAGT 1289

QY 779 TCTGTCCCTATATACACATGAGACCGTCCACTTG 813
DB 1290 TCGTGCCCTTACCAAGTCAACCGCTCGTCTACGTG 1324
RESULT 11
US-09-170-496D-181
Sequence 181, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-C
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 181
LENGTH: 1020
TYPE: DNA
ORGANISM: Homo sapiens
US-09-170-496D-181

Query Match 9.2%; Score 96.2; DB 4; Length 1020;
Best Local Similarity 48.5%; Pred. No. 5.6e-20;
Matches 337; Conservative 0; Mismatches 343; Indels 15; Gaps 2;

QY 119 TTTTCCCAATGTAATCTGATTAATTTTCTGGGAGTCTTGGGAATGGGTTGCCA 178
DB 98 TGTGCGCTCCTCTTACCTTCTGATTTATCTGCTTAGTTGGCAATACCTGGCTC 157
QY 179 TATATGTTTCTCGACGCTTAATAAGATCCACATCTGGAAGCTTTTAACTAAATC 238
DB 158 TGTGCTTTTATCCGAGACCAAGTCCGGACCCCGCAAGTGTCTTATGATC 217
QY 239 TGGGCAATTCAGATCTCTGTTCAATAGACGCTTCCCTTCAGGGCTGATTAATCTTA 298
DB 218 TGGCCGTGGCGGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 277
QY 299 GAGGCTCAATGGATATTTGAGACCTGCGCTGCAAGATTAATGTTCTTATCTTGTATG 358
DB 278 CTGGAAACACTGGCCATTTGGGAAATGCAATGCGTCTTCTTCTTACC 337
QY 359 TCAACATGTAACAGATTAATTTCTGACCGTGTGAGTGTGTCGCTTCTGACCA 418
DB 338 TCAACATGTAACAGATTAATTTCTTCTGACCGTGTGAGTGTGTCGCTTCTGACCA 397
QY 419 TGGTTACCCCTTTCGCTTCTGATGTCAACGATCAAGAGTGCCTGATCTCTGTG 478
DB 398 TTGTGACCCCGGTCAAGTCCCTCAAGCTCGGAGCCCTCTACGACACTGGGCTGTG 457
QY 479 GGAATCATATGATCTTATCATGATGCTTCTCAATATATGCTCTGACATGAGCTGTGAGC 538
DB 458 CCTTCTGT 517
QY 539 AGAAGCGAGTGTACATCATGCTTAAGCTGATCTTAATAATTTGTAAGCTGACA 598
DB 518 TGCAGACCAACCAACGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 577
QY 599 CCATGAACATAATGCTGT 658
DB 578 CCTGTG-----TGTCCCTGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 631
QY 659 GTTATCTGTGATCATTTGGGTTCTGTTAAAGTGAAGTCCAGAAATGGGGCTGGGG 718
DB 632 GCTACCTGTGATCATCCCAAGCTTGGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGT 690
QY 719 TTTTCTACAGAGGACATGACCAACATCATCATCACTTGTATCATCTTCTTGTGTGT 778
DB 691 -----ACCAAGGAGT 742

Qy 779 TCTGCGCTATGACACACTGAGACCGTCCACTTG 813
Db 743 TCTGCGCTATGACACACTGAGACCGTCCACTTG 777

RESULT 12

US-08-097-938-3
Sequence 3, Application US/08097938
Patent No. 5629174
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND ITS
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,938
FILING DATE: 26-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22803-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 56..1249
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 56
US-08-097-938-3

Query Match 8.8%; Score 92; DB 1; Length 1255;
Best Local Similarity 54.4%; Pred. No. 1.4e-18;
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 97 ATTGAAACCTTCAGAGAGAAATTTTCCCAATTGTATATCTGATATATTTTCTGGGGA 156
Db 266 ACTGAAACCTTCAGAGAGAAATTTTCCCAATTGTATATCTGATATATTTTCTGGGGA 325
Qy 157 GTCTTGGGAAATGGGTGTCATATATGTTTCTCGACGCTTATTAAGAGTCACATCT 216
Db 336 TTGCCAAGTAAGGATGGGCTGTCATATATGTTTCTCGACGCTTATTAAGAGTCACATCT 385
Qy 217 GTGAAGCTTTTCATGCTTAATCTGGGCATTTGAGATCTCTGTTATTAAGAGCTTCC 276
Db 386 GCTGATTTTACATGCGCATCTGGCTTGGCTGACCTCTCTGTCATCTGGTTCC 445
Qy 277 TTCAAGGCTGACTATATCTTATAGAGCTCAATTGATATTTGAGAGCCCTGGCTGACG 336
Db 446 TTGAAGATGCTTATCATACATATGCAACAACTGATTTATGGGGAAGCTTTTGTAT 505

Qy 337 ATTATGCTTATCTCTGTATGTCACATGATACAGAGATTTATTTCTGACCGTCTG 396
Db 506 GTGCTTATGCTTTTCTTATGCGAATGATGTCATCTCTTATGATGACCTGCTC 565
Qy 397 AGCTGTGCGCTTTTCTGCGCAATGGTTCAACCCCTTTGGGC 436
Db 566 AGTGTGCAAGGATATGGGTCACTGTAACCCCACTGAGGC 605

RESULT 13

US-08-476-000-3
Sequence 3, Application US/08476000
Patent No. 5716789
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,000
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 56..1249
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 56
US-08-476-000-3

Query Match 8.8%; Score 92; DB 1; Length 1255;
Best Local Similarity 54.4%; Pred. No. 1.4e-18;
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 97 ATTGAAACCTTCAGAGAGAAATTTTCCCAATTGTATATCTGATATATTTTCTGGGGA 156
Db 266 ACTGAAACCTTCAGAGAGAAATTTTCCCAATTGTATATCTGATATATTTTCTGGGGA 325
Qy 157 GTCTTGGGAAATGGGTGTCATATATGTTTCTCGACGCTTATTAAGAGTCACATCT 216
Db 326 TTGCCAAGTAAGGATGGGCTGTCATATATGTTTCTCGACGCTTATTAAGAGTCACATCT 385
Qy 217 GTGAAGCTTTTCATGCTTAATCTGGGCATTTGAGATCTCTGTTATTAAGAGCTTCC 276

Query Match 8.8%; Score 92; DB 2; Length 1255;
Best Local Similarity 54.4%; Pred. No. 1.4e-18;
Matches 185; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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QY 97 ATTGAACCTTCAGAGAGAAATTTTCCCAATTGTATATCTGATTAATATTTTCTGGGGA 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 ACTGGAAACTGACCACTGTCTTCCATTTGTCTACACAATTGTGTGGTGGGT 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 157 GCTTGGGAAATGGGTGTCATATATGTTTCTCGACGCTTATTAAGAAATCCACATCT 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 TTGCCAAGTAAAGGCATGGCCCTGTGGGTCTTCTTTCCGAACTAAGAAAGACACCT 385
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 217 GTGAAGTTTTCATGCTAATATGAGCATTTGAGATCTCCTGTGATTAAGCAAGCTTCCC 276
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 386 GCTGTGATTTACATGGCCCAATCTGGCTTGGCTGACCTCTCTGTGATTTGGTTCCC 445
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 TTCAGGGCTGACTATATCTTAAGAGCTCCAAATTGGATATTGGAGACCTGCTGCAGG 336
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 446 TTGAAGATTGCCATACACATACATGSCAACAACTGSAATTATGGGGAAGCTTTGTAT 505
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 337 ATTATGCTTATTCCTTGATGTCAACATGTAAGCAGTATTATTCTTAACCGTGTG 396
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 506 GTGCTTATTTGCTTTTCTATGSCAACATGTACTGTTCATTCTTCAATGACCTGCTC 565
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 397 AGTGTGTCGCTTCTCGCAATGTTCAACCCCTTGGGC 436
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 566 AGTGTGCAAGGTATTGGGTCACTGAACCCCATGGGC 605
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Search completed: March 20, 2005, 02:59:21
Job time : 208.232 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 19:51:04 ; Search time 4055.5 Seconds
(without alignments)
9770.662 Million cell updates/sec

Title: US-09-826-791a-5

Perfect score: 1041

Sequence: 1 atgagagaaattatcgtc.....gaaggaacaagaactataa 1041

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	723	69.5	758	6	CD630086 56040032J
2	714	68.6	762	6	CD630084 56040024J
3	711	68.3	745	6	CD630072 56039924J
4	709.2	68.1	726	6	CD630089 56040096H
5	693	66.6	720	7	CO959137 AGENCOURT
6	680	65.3	753	6	CD630075 56039988H
7	667.2	64.1	750	6	CD630077 5603996H
8	666	64.0	673	6	CD630069 56039916H
9	655.2	62.9	729	7	CO959148 AGENCOURT
10	651	62.5	652	6	CD630079 56040008H
11	647.4	62.2	670	6	CD630087 56040016H
12	644.8	61.9	663	6	CD630081 56040016H
13	641.4	61.6	682	6	CD630067 56039908H
14	613	58.9	729	7	CF147785 AGENCOURT
15	591	56.8	633	6	CD630066 56039816R
16	588.8	56.6	621	6	CD630074 56039932J
17	550.8	52.9	1739	3	AK008997 Mus muscu
18	521	50.0	844	6	CD630082 56040016J
19	515.6	49.5	860	6	CD630070 56039916J
20	505	48.5	848	6	CD630090 56040096J
21	478.8	46.0	827	6	CD630073 56039932H
22	470.8	45.2	798	6	CD630076 56039988J
23	463	44.5	808	6	CD630088 56040088J
24	457.8	44.0	809	6	CD630068 56039908J

25	439.6	42.2	1015	6	BY754684	BY754684
26	434.6	41.7	620	6	BI961697	BI961697 MONO1.3 D
27	428	41.1	763	6	CD630078	CD630078 5603996J
28	414.4	39.8	740	6	CD630080	CD630080 56040008J
29	412	39.6	735	6	CD630085	CD630085 56040032H
30	404.6	38.9	812	6	CD630071	CD630071 56039924H
31	369.4	35.5	605	4	BI960974	BI960974 MONO1.3 D
32	333	33.0	656	6	CD630083	CD630083 56040024J
33	301.2	28.9	319	8	AQ001459	AQ001459 CTT-HSP-2
34	217.2	20.9	476	5	BX481095	BX481095 DFKP2686J
35	200.4	19.3	604	1	A1178926	A1178926 EST222608
36	147.2	14.1	996	9	CL092116	CL092116 ISB1-2119
37	143.2	13.8	2755	3	AK033476	AK033476 Mus muscu
38	129	12.4	474	2	BF514464	BF514464 UI-H-BW1-
39	125	12.0	833	7	CO919341	CO919341 AGENCOURT
40	123.4	11.9	842	7	CN503141	CN503141 AGENCOURT
41	123.4	11.9	870	7	CO929273	CO929273 AGENCOURT
42	121	11.6	720	7	CF147786	CF147786 AGENCOURT
43	120.4	11.6	666	8	BZ214361	BZ214361 CH230-331
44	116.8	11.2	538	7	CV030948	CV030948 10235 Pul
45	116.4	11.2	671	6	CA376521	CA376521 654906 NC

ALIGNMENTS

RESULT 1
LOCUS CD630086 758 bp mRNA linear EST 12-JAN-2004
DEFINITION 56040032J1 Flp Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630086
VERSION CD630086.1 GI:40278352
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 758)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source location/Qualifiers
1..758

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 69.5%; Score 723; DB 6; Length 758;
Best Local Similarity 98.9%; Pred. No. 2.3e-199;
Matches 749; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

1 ATGAGAGAGAAATTTATGCTTCGCAACCATCTCCGTATCGAATGGAACCAAT 60
2 ATGAGAGAGAAATTTATGCTTCGCAACCATCTCCGTATCGAATGGAACCAAT 61
61 GGCACCTTCAGCAATACACAGCAAGCAATTCACAAATTTCAAGAGATTT 120
62 GGCACCTTCAGCAATACACAGCAAGCAATTCACAAATTTCAAGAGATTT 121
121 TTCCCAATTTATATCTGATTAATATTTTTCGGGAGCTTGGGAATGGGTTTCATTA 180
122 TTCCCAATTTATATCTGATTAATATTTTTCGGGAGCTTGGGAATGGGTTTCATTA 181
181 TATGTTTTCGACACCTTATAGAGTCACATCTGTGAGAGCTTTTCAATGTAATCTG 240

Db 182 TAGTTTCTCGAGCTTTAAGAACTCAGATCTGTAACGTTTTCATGCTAAATCTG 241
QY
QY 241 GCCATTTCAAGATCTCTGTTCTATAGACGCTTCCCTTCAAGGCTGACTATTAATCTTGA 300
Db 242 GCCATTTCAAGATCTCTGTTCTATAGACGCTTCCCTTCAAGGCTGACTATTAATCTTGA 301
QY 301 GGCTCCCAATTGGATTTTGGAGACCTGCTGACGAGATTATGCTTATTTCTGTGATGTC 360
Db 302 GGCTCCCAATTGGATTTTGGAGACCTGCTGACGAGATTATGCTTATTTCTGTGATGTC 361
QY 361 AACATGTACAGCAGATTTATTTCTGACCGTGTGATGTTGCGTTTCTGCGCAATG 420
Db 362 AACATGTACAGCAGATTTATTTTCTGACCGTGTGATGTTGCGTTTCTGCGCAATG 421
QY 421 GTTCAACCCCTTTGGGCTTGTGATGTACACAGATCCAGAGTCCGTGATCTCTGTGGG 480
Db 422 GTTCAACCCCTTTGGGCTTGTGATGTACACAGATCCAGAGTCCGTGATCTCTGTGGG 481
QY 481 ATCATATGATCTTATCATGCGCTTCTCAATAATGCTCTGACAGTGGCTGTGACAG 540
Db 482 ATCATATGATCTTATCATGCGCTTCTCAATAATGCTCTGACAGTGGCTGTGACAG 541
QY 541 AACGGCAGTGTCAATCATGCTTATAGAGCTGATCTTATAAATTTGCTAGTGCAGACC 600
Db 542 AACGGCAGTGTCAATCATGCTTATAGAGCTGATCTTATAAATTTGCTAGTGCAGACC 601
QY 601 ATGAATATATTTGCC-TTGGTGTGGGCTGCTGCTGCTGCAATTTTTCACATCCAGATCTG 659
Db 602 ATGAATATATTTGCC-TTGGTGTGGGCTGCTGCTGCTGCAATTTTTCACATCCAGATCTG 661
QY 660 TTATCTGCTGATCATTCGGGTTCTGTTAAAGTGAGTCCAGATTCGGGGCTGC--GG 717
Db 662 TTATCTGCTGATCATTCGGGTTCTGTTAAAGTGAGTCCAGAAATCGGGGCTGCAGG 721
QY 718 GTTTCTCACAGAGGACCTGACCAACCATCATCATCA 754
Db 722 TTTCTCACAGAGGACCTGACCAACCATCATCATCA 758

RESULT 2
CD630084 762 bp mRNA linear EST 12-JAN-2004
LOCUS 56040024J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630084
ACCESSION CD630084
VERSION CD630084.1 GI:40278350
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 762)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1..762
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1ib="FLP"
/note="Vector: pDrive Cloning Vector"

FEATURES
source

ORIGIN
Query Match 68.6%; Score 714; DB 6; Length 762;
Best Local Similarity 99.5%; Pred. No. 9.7e-197;
Matches 748; Conservative 0; Mismatches 0; Indels 4; Gaps 3;

QY 1 ATGAGAGAAAATTATATGCTTTCAGAACCATCATCTCCGTATCAGAAAAGAACCAAT 60
Db 2 ATGAGAGAAAATTATATGCTTTCAGAACCATCATCTCCGTATCAGAAAAGAACCAAT 61
QY 61 GGCACTTTAGCAATTAACAGCAGAGAACTGCAAAATTGAAAATTCAAGAGAAATT 120
Db 62 GGCACTTTAGCAATTAACAGCAGAGAACTGCAAAATTGAAAATTCAAGAGAAATT 121
QY 121 TTCCCAATTGTATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGTTGTCCATA 180
Db 122 TTCCCAATTGTATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGTTGTCCATA 181
QY 181 TAGTTTCTCGACGCTTATTAAGAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG 240
Db 182 TAGTTTCTCGACGCTTATTAAGAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG 241
QY 241 GCCATTTGAGATCTCTGTTCTATAGACGCTTCCCTCAGGGCTGACTATTAATCTTGA 300
Db 242 GCCATTTGAGATCTCTGTTCTATAGACGCTTCCCTCAGGGCTGACTATTAATCTTGA 301
QY 301 GGCTCCCAATTGGATTTTGGAGACCTGCTGACAGATTATGCTTATTCCTGTATGTC 360
Db 302 GGCTCCCAATTGGATTTTGGAGACCTGCTGACAGATTATGCTTATTCCTGTATGTC 361
QY 361 AACATGTACAGCAGATTTATTTCTGACCGTGTGATGTTGCGTTTCTGCGCAATG 420
Db 362 AACATGTACAGCAGATTTATTTCTGACCGTGTGATGTTGCGTTTCTGCGCAATG 421
QY 421 GTTCAACCCCTTTGGGCTTGTGATGTACACAGATCCAGAGTCCGTGATCTCTGTGGG 480
Db 422 GTTCAACCCCTTTGGGCTTGTGATGTACACAGATCCAGAGTCCGTGATCTCTGTGGG 481
QY 481 ATCATATGATCTTATCATGCGCTTCTCAATAATGCTCTGACAGTGGCTGTGACAG 540
Db 482 ATCATATGATCTTATCATGCGCTTCTCAATAATGCTCTGACAGTGGCTGTGACAG 541
QY 541 AACGGCAGTGTCAATCATGCTTATAGAGCTGATCTTATAAATTTGCTAGTGCAGACC 600
Db 542 AACGGCAGTGTCAATCATGCTTATAGAGCTGATCTTATAAATTTGCTAGTGCAGACC 601
QY 601 ATGAATATATTTGCC-TTGGTGTGGGCTGCTGCTGCTGCAATTTTTCACATCCAGATCTG 659
Db 602 ATGAATATATTTGCC-TTGGTGTGGGCTGCTGCTGCTGCAATTTTTCACATCCAGATCTG 661
QY 660 TTATCTGCTGATCATTCGGGTTCTGTTAAAGTGAGTCCAGATTCGGGGCTGC 716
Db 662 TTATCTGCTGATCATTCGGGTTCTGTTAAAGTGAGTCCAGAAATCGGGGCTGC 721
QY 717 GTTTCTCACAGAGGACCTGACCAACCATCATCA 748
Db 722 GTTTCTCACAGAGGACCTGACCAACCATCATCA 753

RESULT 3
CD630072 745 bp mRNA linear EST 12-JAN-2004
LOCUS 56039924J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630072
ACCESSION CD630072
VERSION CD630072.1 GI:40278338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 745)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102
Email: gfu@incyte.com
Location/Qualifiers
1..745

FEATURES
Source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 68.3%; Score 711; DB 6; Length 745;
Best Local Similarity 99.7%; Pred. No. 7, 2e-196;

Matches 733; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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QY 1 ATGAGAGAAAATTATATGTCCTTGCAACCATTCCTCGATCAGAAAATGAAACCAAT 60
DB 2 ATGAGAGAGAAAATTATATGTCCTTGCAACCATTCCTCGATCAGAAAATGAAACCAAT 61
QY 61 GGACACCTTCAGCAATTAACAACAGCAGAACTGCAATTTGAAAATTCTCAAGAGAAATTT 120
DB 62 GGACACCTTCAGCAATTAACAACAGCAGAACTGCAATTTGAAAATTCTCAAGAGAAATTT 121
QY 121 TTCCCAATTGATATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCCATA 180
DB 122 TTCCCAATTGATATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCCATA 181
QY 181 TATGTTTCTCGAGCCTTATAAGAGTCCATCTGTGAAAGCTTTTCAATGCTAAATCTG 240
DB 182 TATGTTTCTCGAGCCTTATAAGAGTCCATCTGTGAAAGCTTTTCAATGCTAAATCTG 241
QY 241 GCCATTTCAGATCTCTGTCATTAAGCAGGCTTCCCTTCAGGGCTGACTATTAATCTTAAG 300
DB 242 GCCATTTCAGATCTCTGTCATTAAGCAGGCTTCCCTTCAGGGCTGACTATTAATCTTAAG 301
QY 301 GGCTCCAAATTTGATATTTGGAAGCTGGCTGAGAGATTATGCTTAATCTTGTATGTC 360
DB 302 GGCTCCAAATTTGATATTTGGAAGCTGGCTGAGAGATTATGCTTAATCTTGTATGTC 361
QY 361 AACATGTACAGCAGTATTAATTTCTGACCGTGTGAGTGTGTGCGTTCTTGCAATG 420
DB 362 AACATGTACAGCAGTATTAATTTCTGACCGTGTGAGTGTGTGCGTTCTTGCAATG 421
QY 421 GTTCACCCCTTTGCGCTTGTGATGTCACAGCATCAAGATGCTGTGATGCTGTGCG 480
DB 422 GTTCACCCCTTTGCGCTTGTGATGTCACAGCATCAAGATGCTGTGATGCTGTGCG 481
QY 481 ATCATATGATCTTATCATAGGCTTCTCAATTAATGCTCTGGAAGTGCTGTGAGCAG 540
DB 482 ATCATATGATCTTATCATAGGCTTCTCAATTAATGCTCTGTGAGCAG 541
QY 541 AACGGCAGTGTACATCATGCTTGAAGTGAATCTGTATAAATTTGCTAAGCTGACAGC 600
DB 542 AACGGCAGTGTACATCATGCTTGAAGTGAATCTGTATAAATTTGCTAAGCTGACAGC 601
QY 601 ATGAATTAATTTGCTGTTGCG-TGGGCTGCTGCTGCTGCTTTTCAACTCAGACTG 659
DB 602 ATGAATTAATTTGCTGTTGCGCTGTTGCGCTGCTGCTGCTTTTCAACTCAGACTG 661
QY 660 TTATCTGCTGATCATTTGCGGTTCTGTTAA-AGTGAAGTCCAGAAATGGGGCTGCGGG 718
DB 662 TTATCTGCTGATCATTTGCGGTTCTGTTAAAGTGAAGTCCAGAAATGGGGCTGCGGG 721
QY 719 TTTCTCAGAGAAAG 733
DB 722 TTTCTCAGAGAAAG 736
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RESULT 4
CD630089 726 bp mRNA linear EST 12-JAN-2004
LOCUS CD630089 56040096H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630089
ACCESSION

VERSION CD630089.1 GI:40278355
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Fu, G. K., Wang, J. T., Yang, J., Au-Young, J., and Stuve, L. L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES

Source
1..726
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/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 68.1%; Score 709.2; DB 6; Length 726;
Best Local Similarity 99.4%; Pred. No. 2, 4e-195;

Matches 722; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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DB 2 ATGAGAGAGAAAATTATATGTCCTTGCAACCATTCCTCGATCAGAAAATGAAACCAAT 61
QY 61 GGACACCTTCAGCAATTAACAACAGCAGAACTGCAATTTGAAAATTCTCAAGAGAAATTT 120
DB 62 GGACACCTTCAGCAATTAACAACAGCAGAACTGCAATTTGAAAATTCTCAAGAGAAATTT 121
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DB 122 TTCCCAATTGATATCTGATTAATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCCATA 181
QY 181 TATGTTTCTCGAGCCTTATAAGAGTCCATCTGTGAAAGCTTTTCAATGCTAAATCTG 240
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QY 241 GCCATTTCAGATCTCTGTCATTAAGCAGGCTTCCCTTCAGGGCTGACTATTAATCTTAAG 300
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DB 302 GGCTCCAAATTTGATATTTGGAAGCTGGCTGAGAGATTATGCTTAATCTTGTATGTC 361
QY 361 AACATGTACAGCAGTATTAATTTCTGACCGTGTGAGTGTGTGCGTTCTTGCAATG 420
DB 362 AACATGTACAGCAGTATTAATTTCTGACCGTGTGAGTGTGTGCGTTCTTGCAATG 421
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QY 481 ATCATATGATCTTATCATAGGCTTCTCAATTAATGCTCTGGAAGTGCTGTGAGCAG 540
DB 482 ATCATATGATCTTATCATAGGCTTCTCAATTAATGCTCTGTGAGCAG 541
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DB 542 AACGGCAGTGTACATCATGCTTGAAGTGAATCTGTATAAATTTGCTAAGCTGACAGC 601
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QY 661 TATCTGATGATTCGGGTTCTGTTAAAGGAGGATCCAGATCGGGGCTT 720
 Db 661 TATCTGATGATTCGGGTTCTGTTAAAGGAGGATCCAGATCGGGGCTT 720
 QY 721 TCTCAC 726
 Db 721 TCTCAC 726
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 CO959137/c 720 bp mRNA linear EST 17-AUG-2004
 LOCUS AGNCCOURT 30842218 NIH MGC 146 Homo sapiens cDNA clone
 DEFINITION IMAGE:7389737 3', mRNA sequence.
 ACCESSION CO959137
 VERSION CO959137
 KEYWORDS EST.
 SOURCE EST. GI:51323719
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Guthrie cDNA Resource Center
 cDNA Library Preparation: Guthrie cDNA Resource Center
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: IRB17 row: f column: 03
 High quality sequence start: 20
 High quality sequence stop: 632.
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 multiple; ORF's were PCR-amplified (from IMAGE clones or
 from commercially available cDNA libraries) and cloned by
 the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
 into pCDNA3.1. For specific information on cloning sites
 (which vary by clone), please refer to the Guthrie
 website, using the Guthrie ID given in the file
 ftp://image.lnl.gov/image_rearrayed_plates/IRB17.presv.dat
 a. Note: this is a NIH_MGC library."

ORIGIN
 Query Match 66.6%; Score 693; DB 7; Length 720;
 Best Local Similarity 99.9%; Pred. No. 1.3e-190;
 Matches 704; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 336 GATTATGCTTATCTTGTATGTCAACATGTAACAGATTTATTTCTGACCGTGT 395
 Db 720 GATTATGCTTATCTTGTATGTCAACATGTAACAGATTTATTTCTGACCGTGT 661
 QY 396 GAGTGTGTCGTTCTGCGCAATGGTTACCCCTTGGCTTGCATGTCACCAAGAT 455
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 QY 456 CAGAGTGCCTGATCCTGTCGGGATCATATGATCCTTATCATAGGCTTCTCAATAT 515

Db 600 CAGAGTGCCTGATCCTGTCGGGATCATATGATCCTTATCATAGGCTTCTCAATAT 541
 QY 516 GCTCTGTCAGACAGGCTCTGACGAGAACGAGTGCATCATATGCTTGAAGTGAATCT 575
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 QY 576 CTATTAATTTGCTAAGCTGACAGCCATGATATATTTGCTGGTGGGCTGCTGCT 635
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 Db 300 CTGATCATCTTCTTCTGTTCTGTTCTGCTGCTATGACACATGAGACCTTCACCTGAC 241
 QY 816 GACATGAAAGTGGTTATGCAAAAGACAGACTGATTAAGCTTGTATGACCTGGC 875
 Db 240 GACATGAAAGTGGTTATGCAAAAGACAGACTGATTAAGCTTGTATGACCTGGC 181
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 Db 120 TAAGACAGACTAAGTGTGACCTGCAAGAAAGCCATGCAAGAAAGCAAAAGTGT 61
 QY 996 TGTTCCTGCTTGTAGTGTGTTGAGAAAGAAACAAGATTA 1040
 Db 60 TGTTCCTGCTTGTAGTGTGTTGAGAAAGAAACAAGATTA 17
 RESULT 6
 CD630075 753 bp mRNA linear EST 12-JAN-2004
 LOCUS DER10088H1 FLP Homo sapiens cDNA, mRNA sequence.
 DEFINITION CD630075
 ACCESSION CD630075.1 GI:40278341
 VERSION CD630075.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 753)
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
 TITLE Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 JOURNAL Genomics 84 (1), 205-210 (2004)
 COMMENT Contact: Fu GK
 Incyte Genomics, Inc.
 3150 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.

ORIGIN
 Query Match 65.3%; Score 680; DB 6; Length 753;
 Best Local Similarity 98.4%; Pred. No. 8.2e-187;
 Matches 740; Conservative 0; Mismatches 5; Indels 7; Gaps 5;

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 /db_xref="taxon:9606"
 /clone_id="FLP"
 /note="Vector: pDrive Cloning Vector"


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QY 61 GGCACCTTCAGCAATTAACAACAGCAGAGAACTGCACATTTGAAAACCTTCAAGAGAAATTT 120
DB 62 GGCACCTTCAGCAATTAACAACAGCAGAGAACTGCACATTTGAAAACCTTCAAGAGAAATTT 121
QY 121 TTCCCAATTGTATATCTGATTAATATATTTTCTGGGAGCTTGGGAAATGGGTTGCCATA 180
DB 122 TTCCCAATTGTATATCTGATTAATATATTTTCTGGGAGCTTGGGAAATGGGTTGCCATA 181
QY 181 TATGTTTCTCGAGCCTTAATAGAGTCACATCTGTGAACCTTTTCAATGCTAAATCTG 240
DB 182 TATGTTTCTCGAGCCTTAATAGAGTCACATCTGTGAACCTTTTCAATGCTAAATCTG 241
QY 241 GCCATTTCAGATCTCCTGTTCAATAGCAGCTTCCCTCAGGGCTGACTATTAATCTTAA 300
DB 242 GCCATTTCAGATCTCCTGTTCAATAGCAGCTTCCCTCAGGGCTGACTATTAATCTTAA 301
QY 301 GGCTCCCAATTGTATATTTGAGACCTGCGCTGAGGATTAATGCTTATTTCTTGTATGTC 360
DB 302 GGCTCCCAATTGTATATTTGAGACCTGCGCTGAGGATTAATGCTTATTTCTTGTATGTC 361
QY 361 AACATGTACAGAGATTAATTTATTTCTCGACCGCTGAGCTGAGTGTGGCTTCTCGGCAATG 420
DB 362 AACATGTACAGAGATTAATTTATTTCTCGACCGCTGAGCTGAGTGTGGCTTCTCGGCAATG 421
QY 421 GTTCAACCCCTTTCGCGCTTGCATGTCACACAGCATCAGAGATGCTGAAATCTCTGTGG 480
DB 422 GTTCAACCCCTTTCGCGCTTGCATGTCACACAGCATCAGAGATGCTGAAATCTCTGTGG 481
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DB 482 ATCATATGATCTTATCATAGCTTCTCTCAATATGCTCTGAGCAGTGCCTGAGCAG 541
QY 541 AACGGCAGTGTACATCATGCTTAAAGCTGAAATCTCTA-TAAATGCTTAAGTGCAGAGC 599
DB 542 AACGGCAGTGTACATCATGCTTAAAGCTGAAATCTCTA-TAAATGCTTAAGTGCAGAGC 601
QY 600 CATGAACCTATATTTGCTGTGTGGTGGCTGCTGCTGCA-TTTTTCACATCAGCATCT 658
DB 602 CATGAACCTATATTTGCTGTGTGGTGGCTGCTGCTGCA-TTTTTCACATCAGCATCT 661
QY 659 GTTATCTG-CTGATCATTTGGGTTCTGTTAAAGTGAAGTCCAGAAATCGGGGCTGCG 717
DB 662 GTTATCTGCTGATCATTTGGGTTCTGTTAAAGTGAAGT-CCAGAAATCGGGGCTGCG 720
QY 718 GTTTCTC--ACAGAGAGCATGACCAACAT 746
DB 721 GGTTCTCACAAGAGCATGACCAACAT 752

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RESULT 7
LOCUS CD630077 750 bp mRNA linear EST 12-JAN-2004
DEFINITION 56039916H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630077
VERSION CD630077.1 GI:40278343
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 750)
AUTHORS Fu G.K., Wang J.T., Yang J., Au-Young J. and Strive L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extenslon cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102
Email: gfu@incyte.com
Location/Qualifiers
FEATURES
source
1..750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_id="FLP"
/note="Vector: pDrive Cloning Vector"

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Query Match 64.1%; Score 667.2; DB 6; Length 750;
Best Local Similarity 97.5%; Pred. No. 4.5e-183;
Matches 731; Conservative 0; Mismatches 13; Indels 6; Gaps 5;

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QY 61 GGCACCTTCAGCAATTAACAACAGCAGAGAACTGCACATTTGAAAACCTTCAAGAGAAATTT 120
DB 62 GGCACCTTCAGCAATTAACAACAGCAGAGAACTGCACATTTGAAAACCTTCAAGAGAAATTT 121
QY 121 TTCCCAATTGTATATCTGATTAATATATTTTCTGGGAGCTTGGGAAATGGGTTGCCATA 180
DB 122 TTCCCAATTGTATATCTGATTAATATATTTTCTGGGAGCTTGGGAAATGGGTTGCCATA 181
QY 181 TATGTTTCTCGAGCCTTAATAGAGTCACATCTGTGAACCTTTTCAATGCTAAATCTG 240
DB 182 TATGTTTCTCGAGCCTTAATAGAGTCACATCTGTGAACCTTTTCAATGCTAAATCTG 241
QY 241 GCCATTTCAGATCTCCTGTTCAATAGCAGCTTCCCTCAGGGCTGACTATTAATCTTAA 300
DB 242 GCCATTTCAGATCTCCTGTTCAATAGCAGCTTCCCTCAGGGCTGACTATTAATCTTAA 301
QY 301 GGCTCCCAATTGTATATTTGAGACCTGCGCTGAGGATTAATGCTTATTTCTTGTATGTC 360
DB 302 GGCTCCCAATTGTATATTTGAGACCTGCGCTGAGGATTAATGCTTATTTCTTGTATGTC 361
QY 361 AACATGTACAGAGATTAATTTATTTCTGACCGCTGAGCTGAGTGTGGCTTCTCGGCAATG 420
DB 362 AACATGTACAGAGATTAATTTATTTCTGACCGCTGAGCTGAGTGTGGCTTCTCGGCAATG 421
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QY 541 AACGGCAGTGTACATCATGCTTAAAGCTGAAATCTCTA-TAAATGCTTAAGTGCAGAGC 598
DB 542 AACGGCAGTGTACATCATGCTTAAAGCTGAAATCTCTA-TAAATGCTTAAGTGCAGAGC 601
QY 599 CCATGAACCTATATTTGCTGTGTGGTGGCTGCTGCTGCA-TTTTTCACATCAGCATCT 658
DB 602 CCATGAACCTATATTTGCTGTGTGGTGGCTGCTGCTGCA-TTTTTCACATCAGCATCT 660
QY 659 GTTATCTGCTGATCATTTGGGTTCTGTTAAAGTGAAGTCCAGAAATCGGGGCTGCG 717
DB 661 GTTATCTGCTGATCATTTGGGTTCTGTTAAAGTGAAGTCCAGAAATCGGGGCTGCG 720
QY 718 G--TTTCTCAGAGAGCATGACCAACA 745
DB 721 GGTTCTCACAAGAGCATGACCAACA 750

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RESULT 8
LOCUS CD630069 673 bp mRNA linear EST 12-JAN-2004
DEFINITION 56039916H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630069

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VERSION      CD630069.1  GI:40278335
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE    1 (bases 1 to 673)
              Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
              Circular rapid amplification of cDNA ends for high-throughput
              extension cloning of partial genes
              Genomics 84 (1), 205-210 (2004)
JOURNAL
COMMENT      Contact: Fu GK
              Incyte Genomics, Inc.
              3160 Porter Dr., Palo Alto, CA 94304, USA
              Tel: 6508454102
              Email: gfu@incyte.com.
FEATURES
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    /organism="Homo sapiens"
    /mol_type="mRNA"
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    /clone_lib="PLP"
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Query Match      64.0%; Score 666; DB 6; Length 673;
Best Local Similarity 100.0%; Pred. No. 9, 6e-183;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGAGAGAAAATTATGCTCTTGCAACATCCATCCCTGATCAGAAATGAAACCAAT 60
DB      2  ATGAGAGAAAATTATGCTCTTGCAACATCCATCCCTGATCAGAAATGAAACCAAT 61
QY      61  GGACCTTCAGCAATAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB      62  GGACCTTCAGCAATAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 121
QY      121  TTCCCAATTGATATCTGATATATTTTCTGGGAGCTCTTGAGAAATGGGTTGTCATA 180
DB      122  TTCCCAATTGATATCTGATATATTTTCTGGGAGCTCTTGAGAAATGGGTTGTCATA 181
QY      181  TAGTTTTCTGAGAGCTTTAAGAAATCCACATCTGTGAAGCTTTTCACTGAATCTG 240
DB      182  TAGTTTTCTGAGAGCTTTAAGAAATCCACATCTGTGAAGCTTTTCACTGAATCTG 241
QY      241  GCCATTTCAGATCTCTGTCATAGACAGCTTCCCTTGAGGCTGACATTAATCTTAA 300
DB      242  GCCATTTCAGATCTCTGTCATAGACAGCTTCCCTTGAGGCTGACATTAATCTTAA 301
QY      301  GGCTCCAAATGATATTTGAGAGCTGGCTGAGAGATTAATGTTATTTCTTGTATGTC 360
DB      302  GGCTCCAAATGATATTTGAGAGCTGGCTGAGAGATTAATGTTATTTCTTGTATGTC 361
QY      361  AACATGTAACAGATATTTATTTCTGACCGTGTAGTGTGCTTCCCTGGAAG 420
DB      362  AACATGTAACAGATATTTATTTCTGACCGTGTAGTGTGCTTCCCTGGAAG 421
QY      421  GTTCAACCCCTTGGCTTGCATGTACACAGAGATGAGAGAGAGAGAGAGAGAGAGAG 480
DB      422  GTTCAACCCCTTGGCTTGCATGTACACAGAGATGAGAGAGAGAGAGAGAGAGAGAG 481
QY      481  ATCATATGATCTTATCATGCTTCTCAATATATCTCTTGACAGTGGCTTGAAGAG 540
DB      482  ATCATATGATCTTATCATGCTTCTCAATATATCTCTTGACAGTGGCTTGAAGAG 541
QY      541  AACGGAGTGTACATCATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB      542  AACGGAGTGTACATCATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601
QY      601  ATGAATATATATGCTTGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB      602  ATGAATATATATGCTTGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661

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QY      661  TATCTG 666
DB      662  TATCTG 667

RESULT 9
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DEFINITION  CO959148 729 bp mRNA linear EST 17-AUG-2004
AGENCOURT 30842618 NIH MGC_146 Homo sapiens cDNA clone
IMAGE:7389737 5', mRNA sequence.
ACCESSION  CO959148
VERSION    CO959148.1  GI:51323730
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE  NIH-MGC http://mgi.nci.nih.gov/.
              1 (bases 1 to 729)
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Daniela S. Gerhard, Ph.D.
              Office of Cancer Genomics
              National Cancer Institute / NIH
              Bldg. 31 Rm10A07 Bethesda, MD 20892
              Email: cgsabhs-remail.nih.gov
              Tissue Procurement: Guthrie cDNA Resource Center
              cDNA Library Preparation: Guthrie cDNA Resource Center
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              plate: IRB17 row: E column: 03
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    1..729
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    /clone_lib="NIH MGC 146"
    /note="Vector: pCDNA3.1; Site 1: multiple; Site 2:
    multiple; ORF's were PCR-amplified (from IMAGE clones or
    from commercially available cDNA libraries) and cloned by
    the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
    into pCDNA3.1. For specific information on cloning sites
    (which vary by clone), please refer to the Guthrie
    website, using the Guthrie ID given in the file
    ftp://image.llnl.gov/image_rearrayed_plates/IRBP_presv.dat
    a. Note: this is a NIH_MGC Library."
ORIGIN
Query Match      62.9%; Score 655.2; DB 7; Length 729;
Best Local Similarity 95.1%; Pred. No. 1, 4e-179;
Matches 696; Conservative 0; Mismatches 32; Indels 4; Gaps 2;

QY      1  ATGAGAGAAAATTATGCTCTTCAACCATCTCCGTATCAGAAATGAAACCAAT 60
DB      2  ATGAGAGAAAATTATGCTCTTCAACCATCTCCGTATCAGAAATGAAACCAAT 61
QY      61  GGACCTTCAGCAATAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB      62  GGACCTTCAGCAATAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 121
QY      121  TTCCCAATTGATATCTGATATATTTTCTGGGAGCTTTGGGAAATGGGTTGTCATA 180
DB      122  TTCCCAATTGATATCTGATATATTTTCTGGGAGATCTTTGGGAAATGGGTTGTCATA 181
QY      181  TAGTTTTCTGAGAGCTTTAAGAAATCCACATCTGTGAAGCTTTTCATGCTTAATCTG 240

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Db 182 TATGTTTCCCTGACGCTTATAGAAGTCCACATCTGTGAAGCTTTTCATGCTAAATCTG 241
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Db 242 GGCATTTTCAGATCTCTGTTCAATAGCAGCTTCCCTTACGGCTGACATATATCTTAA 301
Qy 301 GGCCTCAATTGGATATTTGGAGACCTGGCTGACAGATTATGCTTATCTTATATGTC 360
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Db 482 ATCATATGGATCTTATCATAGGCTTCTCATATATGCTCTGGAACAGTCTGTGAGAG 541
Qy 541 AACGGCAGTGCATCATCATGCTTAAAGCTGAACTCTTATAAATTGCTAAAGCTGACAG 600
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Qy 601 ATGAACATATATGCTTGTGCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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Qy 661 TATGCTGATCATCTCGGGTCTGTTAAAGAGTCCAGAAATCGGGAGCTGGGGGT 720
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Qy 721 TCTCAGAGAG 732
Db 718 TCACAAAGAAAG 729

RESULT 10
CD630079 652 bp mRNA linear EST 12-JAN-2004
LOCUS 56040008H1 FLB Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630079
ACCESSION CD630079.1 GI:40278345
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 652)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1. 652
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/note="Vector: pDrive Cloning Vector"

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Query Match 62.5%; Score 651; DB 6; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.3e-178;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGAAATTTATGTCCTTGAACCATCCATCTCCGTATCAGAAATGGAAACCAAT 60
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Qy 241 GCCATTTCAGATCTCTGTTCAATAGCAGCTTCCCTTACGGCTGACATATATCTTAA 300
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RESULT 11
CD630087 670 bp mRNA linear EST 12-JAN-2004
LOCUS 56040008H1 FLB Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630087
ACCESSION CD630087.1 GI:40278353
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 670)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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ORIGIN

Query Match 62.2%; Score 647.4; DB 6; Length 670;
 Best Local Similarity 99.7%; Pred. No. 2.6e-177;
 Matches 659; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 ATGAGAGAAAATTTATGCTCTTGAACCATCATCTCCGTATCAGAAATGGAACCAAT 60
 DB 2 ATGAGAGAAAATTTATGCTCTTGAACCATCATCTCCGTATCAGAAATGGAACCAAT 61
 QY 61 GGCACTTCAGCAATPAACAACAGCAGAACTGCAATGAAAATCTCAAGAGAAATTT 120
 DB 62 GGCACTTCAGCAATPAACAACAGCAGAACTGCAATGAAAATCTCAAGAGAAATTT 121
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 DB 182 TATGTTTCTCGAGCTTATTAAGAAGTCCATCTGTGAACGTTTCAATGCTAAATCTG 241
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 QY 601 ATGAATCTATATGCTTGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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 QY 661 T 661
 DB 661 T 661

RESULT 12
 LOCUS CD630081 663 bp mRNA linear EST 12-JAN-2004
 DEFINITION 56040016H1 FLP Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD630081
 VERSION CD630081.1 GI:40278347
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 663)
 Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
 Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 Genomics 84 (1), 205-210 (2004)
 JOURNAL CONTACT: Fu GK
 COMMENT Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com
 Location/Qualifiers
 1..663
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /note="Vector: pDrive Cloning Vector"

FEATURES

source

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Query Match 61.9%; Score 644.8; DB 6; Length 663;
 Best Local Similarity 99.4%; Pred. No. 1.5e-176;
 Matches 658; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1 ATGAGAGAAAATTTATGCTCTTGAACCATCATCTCCGTATCAGAAATGGAACCAAT 60
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 DB 62 GGCACTTCAGCAATPAACAACAGCAGAACTGCAATGAAAATCTCAAGAGAAATTT 121
 QY 121 TTCCCAATGTATCTGATTAATTTTCTGGGAGCTTGGGAATGGCTTGCATTA 180
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 QY 181 TATGTTTCTCGAGCTTATTAAGAAGTCCATCTGTGAACGTTTCAATGCTAAATCTG 240
 DB 182 TATGTTTCTCGAGCTTATTAAGAAGTCCATCTGTGAACGTTTCAATGCTAAATCTG 241
 QY 241 GCCATTCAGATCTCTGTTCAATAGCAGCTTCCCTTCAAGGCTGACTATTAATCTTAA 300
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 QY 301 GGCTCCAATTTGATTTTGAAGCCTGGCTGAGATTAATGCTTAATCTTGAATGTC 360
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 QY 361 AACATGTACAGAGATTTATTTCTGACCGTGTAGTGTGGCTTCTGCAATG 420
 DB 362 AACATGTACAGAGATTTATTTCTGACCGTGTAGTGTGGCTTCTGCAATG 421
 QY 421 GTTCACCCCTTGGCTTCTGATGTACAGCATAGAGTCTGTGATCTTGTGG 480
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 QY 481 ATCATATGATCTTATCATAGGCTTCTCAATTAATGCTCTGAGAGTCTGAGCAG 540
 DB 482 ATCATATGATCTTATCATAGGCTTCTCAATTAATGCTCTGAGAGTCTGAGCAG 541
 QY 541 AACGGCAGTGCATCATAGCTTGAAGCTGAATCTCTAATAATGCTAAGCTGACAGC 600
 DB 542 AACGGCAGTGCATCATAGCTTGAAGCTGAATCTCTAATAATGCTAAGCTGACAGC 601
 QY 601 ATGAATCTATATGCTTGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 658
 DB 602 ATGAATCTATATGCTTGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
 QY 659 GT 660
 DB 662 GT 663

RESULT 13
 LOCUS CD630067 682 bp mRNA linear EST 12-JAN-2004
 DEFINITION 56039908H1 FLP Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD630067
 VERSION CD630067.1 GI:40278333
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS Pu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 94 (1), 205-210 (2004)
COMMENT Contact: Pu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com

FEATURES
source location/Qualifiers
1..682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1ib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 61.6%; Score 641.4; DB 6; Length 682;
Best Local Similarity 97.4%; Pred. No. 1.5e-175;
Matches 663; Conservative 0; Mismatches 16; Indels 2; Gaps 1;

QY 1 ATGAGAGAAAATTTATGCTTTCGACATCCATCTCCGATCAGAAATGAAACCAAT 60
DB 2 ATGAGAGAAAATTTATGCTTTCGACATCCATCTCCGATCAGAAATGAAACCAAT 61
QY 61 GGCACCTTCAGCAATTAACAAGCAGCACTGCAATGAAACTTCAAGAGAAATT 120
DB 62 GGCACCTTCAGCAATTAACAAGCAGCACTGCAATGAAACTTCAAGAGAAATT 121
QY 121 TTCCCAATTGATATCTGATTAATATTTTCTGGAGAGCTTGGGAAATGGATTGTCATA 180
DB 122 TTCCCAATTGATATCTGATTAATATTTTCTGGAGAGCTTGGGAAATGGATTGTCATA 181
QY 181 TATGTTTCTCGACGCTTATAAAGATCCACATCTGTGAACGTTTCAATGCTAAATCTG 240
DB 182 TATGTTTCTCGACGCTTATAAAGATCCACATCTGTGAACGTTTCAATGCTAAATCTG 241
QY 241 GGCATTTGAGTCTCTGTTCAATAGCAGGCTTCCCTTCAAGGCTGACATATCTTAA 300
DB 242 GGCATTTGAGTCTCTGTTCAATAGCAGGCTTCCCTTCAAGGCTGACATATCTTAA 301
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QY 361 AACATGTACAGCAGATTTATTTCTGACCGTCTGAGGTTGTGGCTTCTGGCAATG 420
DB 362 AACATGTACAGCAGATTTATTTCTGACCGTCTGAGGTTGTGGCTTCTGGCAATG 421
QY 421 GTTACACCCCTTTCGGCTTCTGCATGTCAACAGCATAGAGAGTCTGTGGG 480
DB 422 GTTACACCCCTTTCGGCTTCTGCATGTCAACAGCATAGAGAGTCTGTGGG 481
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DB 482 ATCATATGGAATCTTATCATAGGCTTCTGAATTAATGCTCTGGAACAGGCTCTGAGC 541
QY 541 AACGGCAGTGTACATCATGCTTAAAGCTAAATCTCTATMAAA--TTGCTAAAGCTGACAG 598
DB 542 AACGGCAGTGTACATCATGCTTAAAGCTAAATCTCTATMAAAATGCTTAAGCTGACAG 601
QY 599 CCATGAACATATATGCTTGT 658
DB 602 CCATGAACATATATGCTTGT 661
QY 659 GTTATCTGCTGATCATTTGGG 679
DB 662 GTTATCTGCTGATCATTTGGG 682

RESULT 14
CF147785 729 bp mRNA linear EST 25-JUL-2003
LOCUS AGENCOURT 14740193 NIH MGC 145 Homo sapiens cDNA clone
DEFINITION IMAGE:6971946 5', mRNA sequence.
ACCESSION CF147785
VERSION CF147785.1 GI:33244053
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 729)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBI02 row: f column: 05
High quality sequence stop: 659.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971946"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_1ib="NIH MGC 145"
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-Xmi1/Xho1-3',
5'-EcoRV-Xmi1/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/earrayed_plates/IRBI.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 58.9%; Score 613; DB 7; Length 729;
Best Local Similarity 100.0%; Pred. No. 3e-167;
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGAAAATTTATGCTTTCGACATCCATCTCCGATCAGAAATGAAACCAAT 60
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QY 61 GGCACCTTCAGCAATTAACAAGCAGCACTGCAATGAAACTTCAAGAGAAATT 120
DB 177 GGCACCTTCAGCAATTAACAAGCAGCACTGCAATGAAACTTCAAGAGAAATT 236
QY 121 TTCCCAATTGATATCTGATTAATATTTTCTGGAGAGCTTGGGAAATGGATTGTCATA 180
DB 237 TTCCCAATTGATATCTGATTAATATTTTCTGGAGAGCTTGGGAAATGGATTGTCATA 296
QY 181 TATGTTTCTCGACGCTTATAAAGATCCACATCTGTGAACGTTTCAATGCTAAATCTG 240
DB 297 TATGTTTCTCGACGCTTATAAAGATCCACATCTGTGAACGTTTCAATGCTAAATCTG 356
QY 241 GGCATTTGAGTCTCTGTTCAATAGCAGCTTCCCTTCAAGGCTGACATATATCTTAA 300

Db 357 GCATTTCGATCTCTGTTCAATAGACGCTTCCCTTCAAGGCTGACTATATCTTAA 416
Qy 301 GGCTCCAAATGGATATTTGGAGACCTGGCTGCAGAGATTATGCTTATTCCTGTATGTC 360
Db 417 GGCTCCAAATGGATATTTGGAGACCTGGCTGCAGAGATTATGCTTATTCCTGTATGTC 476
Qy 361 AACATGTACAGAGATATTTATTTCTGACCGGTGCTAGAGTTGGGTTTCCGGCAATG 420
Db 477 AACATGTACAGAGATATTTATTTCTGACCGGTGCTAGAGTTGGGTTTCCGGCAATG 536
Qy 421 GTTCAACCCCTTTCGGCTTTCGATGTACACAGCATCAGAGTGCCTGATCTCTGTGGG 480
Db 537 GTTCAACCCCTTTCGGCTTTCGATGTACACAGCATCAGAGTGCCTGATCTCTGTGGG 596
Qy 481 ATCATATGTGATCTTATATCATGCTTCTCTCAATATAGTCTCTGACAGTGGCTTGAAGCAG 540
Db 597 ATCATATGTGATCTTATATCATGCTTCTCTCAATATAGTCTCTGACAGTGGCTTGAAGCAG 656
Qy 541 AACGGAGGTGCATCATGCTTGAAGCTGAATCTCTAATAATTGCTAAGCTGCAGACC 600
Db 657 AACGGAGGTGCATCATGCTTGAAGCTGAATCTCTAATAATTGCTAAGCTGCAGACC 716
Qy 601 ATGAACCTATATTG 613
Db 717 ATGAACCTATATTG 729

RESULT 15

CD630066 633 bp mRNA linear EST 12-JAN-2004
LOCUS 56039816R6 FLP Homo sapiens cDNA, mRNA sequence.
DERIVATION CD630066
ACCESSION CD630066
VERSION CD630066.1 GI:40278332
KEYWORDS EST.

SOURCE

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

JOURNAL

Genomics 84 (1), 205-210 (2004)

Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES

Location/Qualifiers
1..633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 56.8%; Score 591; DB 6; Length 633;
Best Local Similarity 99.8%; Pred. No. 7.5e-161;
Matches 602; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGGAGAGAAATTTATGTCCTTGGCAACATCATCTCCGTATCAGAAATGGAAACCAAT 60
Db 2 ATGGAGAGAAATTTATGTCCTTGGCAACATCATCTCCGTATCAGAAATGGAAACCAAT 61
Qy 61 GGACACCTTCAGCAATACAGACAGAGAACTGCACAAATGAAATCTCAAGAGAGAAATTT 120
Db 62 GGACACCTTCAGCAATACAGACAGAGAACTGCACAAATGAAATCTCAAGAGAGAAATTT 121
Qy 121 TTCCCAATTGTATATCTGATATATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCCATA 180
Db 122 TTCCCAATTGTATATCTGATATATATTTTCTGGGAGTCTTGGGAAATGGGTTGTCCATA 181

Qy 181 TATGTTTCCCTGACGCTTATTAAGAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG 240
Db 182 TATGTTTCCCTGACGCTTATTAAGAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG 241
Qy 241 GCCATTTTCAGATCTCTGTTCAATGAACAGCTTCCCTTCAGGGCTGACTATATCTTGA 300
Db 242 GCCATTTTCAGATCTCTGTTCAATGAACAGCTTCCCTTCAGGGCTGACTATATCTTGA 301
Qy 301 GGCTCCAAATGGATATTTGGAGACCTGGCTGCTGAGAGTTATGCTTATTCCTGTATGTC 360
Db 302 GGCTCCAAATGGATATTTGGAGACCTGGCTGCTGAGAGTTATGCTTATTCCTGTATGTC 361
Qy 361 AACATGTACAGAGATATTTATTTCTGACCGGTGCTAGAGTTGGGTTTCCGGCAATG 420
Db 362 AACATGTACAGAGATATTTATTTCTGACCGGTGCTAGAGTTGGGTTTCCGGCAATG 421
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Db 422 GTTCAACCCCTTTCGGCTTTCGATGTACACAGCATCAGAGTGCCTGATCTCTGTGGG 481
Qy 481 ATCATATGTGATCTTATATCATGCTTCTCTCAATATAGTCTCTGACAGTGGCTTGAAGCAG 540
Db 482 ATCATATGTGATCTTATATCATGCTTCTCTCAATATAGTCTCTGACAGTGGCTTGAAGCAG 541
Qy 541 AACGGAGGTGCATCATGCTTGAAGCTGAATCTCTAATAATTGCTAAGCTGCAGAC 599
Db 542 AACGGAGGTGCATCATGCTTGAAGCTGAATCTCTAATAATTGCTAAGCTGCAGAC 601
Qy 600 CAT 602
Db 602 CAT 604

Search completed: March 20, 2005, 02:52:32
Job time : 4057.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2005, 16:09:56 ; Search time 30.7544 Seconds
(without alignments)
800.996 Million cell updates/sec

Title: US-09-826-791A-2

Perfect score: 1712

Sequence: 1 MERNPTFSNNRNCTIENF.....KAKTKCVFVSVWLAKITRV 330

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1703	99.5	346	4	US-09-585-876-2
2	559	32.7	337	3	US-09-044-404A-2
3	559	32.7	337	4	US-09-586-924-2
4	479	28.0	339	1	US-08-153-848-44
5	479	28.0	339	2	US-08-812-871-3
6	479	28.0	339	3	US-09-899-843A-44
7	479	28.0	339	3	US-09-088-337B-44
8	479	28.0	339	4	US-09-170-496D-32
9	479	28.0	339	5	PCT-US93-11153-44
10	479	28.0	339	5	PCT-US95-07180-2
11	476	27.8	339	4	US-09-170-496D-182
12	461	26.9	362	3	US-08-513-974B-374
13	446	26.1	373	4	US-09-745-842-14
14	442	25.8	373	2	US-08-559-524A-4
15	442	25.8	373	3	US-08-749-707-4
16	442	25.8	373	4	US-09-947-922-4
17	440	25.7	361	1	US-08-383-750-4
18	440	25.7	361	1	US-08-352-678-4
19	440	25.7	361	4	US-09-536-954-4
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22	440	25.7	361	5	PCT-US93-09636-4
23	439.5	25.7	348	3	US-08-852-824-17
24	439	25.6	302	2	US-08-467-948A-30
25	439	25.6	302	2	US-08-467-947A-30
26	437	25.5	344	2	US-08-467-948A-8
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28	434	25.4	361	4	US-09-170-496D-206	Sequence 206, App
29	434	25.4	377	4	US-09-745-842-17	Sequence 17, Appl
30	430	25.1	370	3	US-08-781-250-2	Sequence 2, Appl1
31	424.5	24.8	374	4	US-09-745-842-15	Sequence 15, Appl
32	419.5	24.5	373	4	US-09-102-710B-3	Sequence 3, Appl1
33	416.5	24.3	373	3	US-08-513-974B-173	Sequence 373, App
34	416	24.3	342	3	US-08-988-876-9	Sequence 9, Appl1
35	416	24.3	375	1	US-08-442-134A-2	Sequence 2, Appl1
36	416	24.3	375	1	US-08-444-581B-2	Sequence 2, Appl1
37	416	24.3	375	1	US-08-446-088A-2	Sequence 2, Appl1
38	416	24.3	375	1	US-08-559-524A-3	Sequence 3, Appl1
39	416	24.3	375	4	US-08-749-707-3	Sequence 3, Appl1
40	416	24.3	375	4	US-09-947-922-3	Sequence 3, Appl1
41	409.5	23.9	342	4	US-09-054-272-2	Sequence 2, Appl1
42	406.5	23.7	398	1	US-08-097-938-6	Sequence 6, Appl1
43	406.5	23.7	398	1	US-08-476-000-6	Sequence 6, Appl1
44	406.5	23.7	398	1	US-08-472-840-6	Sequence 6, Appl1
45	406.5	23.7	398	2	US-08-476-976-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-585-876-2

Sequence 2, Application US/09585876

Patent No. 6586205

GENERAL INFORMATION:

APPLICANT: Glucksmann, Maria Alexandra

APPLICANT: Siloe-Santiago, Immaculada

TITLE OF INVENTION: 43239, A No. 6586205e1 GPCC-Like Molecule and

FILE REFERENCE: 5800-88

CURRENT APPLICATION NUMBER: US/09/585,876

CURRENT FILING DATE: 2000-06-01

EARLIER APPLICATION NUMBER: 60/182,061

EARLIER FILING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 346

TYPE: PRT

ORGANISM: Homo sapiens

US-09-585-876-2

Query Match 99.5%; Score 1703; DB 4; Length 346;

Best Local Similarity 99.4%; Pred. No. 3, 7e-124;

Matches 328; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY	61	MNLAIIDLFFSTLPFRADYYLRGSNWF	FGDLACRINSYSLYVMNYSIYFLTVLSVR	120
DB	77	MNLAIIDLFFSTLPFRADYYLRGSNWF	FGDLACRINSYSLYVMNYSIYFLTVLSVR	136
QY	121	FLAMVHPRFLVHTSIRSAMI	LCGIIWILIMASSIMLDSGEQNGSVTSCLEMLYKIA	180
DB	137	FLAMVHPRFLVHTSIRSAMI	LCGIIWILIMASSIMLDSGEQNGSVTSCLEMLYKIA	196
QY	181	KIQTMNYIALVVGCLLPFTLS	ICYLLIRVLAKYEVPPSSGRVSRKALLTTIIITLIIF	240
DB	197	KIQTMNYIALVVGCLLPFTLS	ICYLLIRVLAKYEVPPSSGRVSRKALLTTIIITLIIF	256
QY	241	FLCPLPYHTLRVHTLTTVMV	GLCKDRLHKALVITTLAANA	CNPDLTYYPAGENFKDRL 300
DB	257	FLCPLPYHTLRVHTLTTVMV	GLCKDRLHKALVITTLAANA	CNPDLTYYPAGENFKDRL 316
QY	301	KSALRKGHQKAKTKCVFVSV	WMLRKETRV 330	
DB	317	KSALRKGHQKAKTKCVFVSV	WMLRKETRV 346	

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RESULT 2
US-09-044-404a-2
; Sequence 2, Application US/09044404A
; Patent No. 6200775
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: AMES, ROBERT
; APPLICANT: FOLEY, JAMES
; APPLICANT: SARAU, HENRY
; TITLE OF INVENTION: CDNA CLONE HMTW81 THAT ENCODES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 790 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,404A
; FILING DATE: MARCH 19, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,795
; FILING DATE: APRIL 22, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T.
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH-70001-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-044-404A-2

Query Match          32.7%; Score 559; DB 3; Length 337;
Best Local Similarity 38.0%; Pred. No. 7.7e-36;
Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;

QY 11 NSRNC--TIENFKREFPIVYLIIFWGVLGNGLSIVFLOPYKKSSTVNVFMNLAI5D 68
DB 10 SSATCHDTIDDFRNOVYVSTLYSMISVGFNGFVLYVLIKTHKSAFOVYMINLAVAD 69
QY 69 LIFSTLPFRADYLYLRSGNWIFGDLACRIMSYSLVNMYSIYFLVLSVRFAMVHPF 128
DB 70 LVCVCTLPFRVYVYVYHKGIMLFGDFLCRLSTYALVNLCSIFEMTMSFFRCIAIVFPV 129
QY 129 RLHVTISRASAMILGIIWI-LIMASSIMLLDGSSENGSVTSCLEINLYKIAK--LQTM 185
DB 130 QNINLVTOKKARFVCVGIWIFVILITSSPFLMAKPKQDKGNNTKCEPPQDNQTKNHVVL 189
QY 186 NYIALVVGCLLPFTLSICVYLIIRVLKVEVBSGLRVSHRKALTTIITLIIFLCFL 245
DB 190 HVSLSFVGFIIFPVIIIVCYTMIITLLKSKMKN--LSHKKALGIMIVVTAFLVSFM 247
QY 246 PYHTLRVHLTTW--KVGICKD--RLHRAVLTTLAANAACPNFLVYPAGENFKORLK 301
DB 307 STFRK 311
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DB 248 PYHIOHTIHLFHLNETKPCDSVLRMQKSVITLTLAASNCCEPDLTYFFSGGNFRKRL- 306
QY 302 SALRK 306
DB 307 STFRK 311

RESULT 3
US-09-586-924-2
; Sequence 2, Application US/09586924
; Patent No. 6506878
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH M.
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: AMES, ROBERT S.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: CHAMBERS, JON
; TITLE OF INVENTION: CDNA CLONE HMTW81 THAT ENCODES A NOVEL
; FILE REFERENCE: GH-70001-1D1
; CURRENT APPLICATION NUMBER: US/09/586,924
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 09/044,404
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/844,795
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-586-924-2

Query Match          32.7%; Score 559; DB 4; Length 337;
Best Local Similarity 38.0%; Pred. No. 7.7e-36;
Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;

QY 11 NSRNC--TIENFKREFPIVYLIIFWGVLGNGLSIVFLOPYKKSSTVNVFMNLAI5D 68
DB 10 SSATCHDTIDDFRNOVYVSTLYSMISVGFNGFVLYVLIKTHKSAFOVYMINLAVAD 69
QY 69 LIFSTLPFRADYLYLRSGNWIFGDLACRIMSYSLVNMYSIYFLVLSVRFAMVHPF 128
DB 70 LVCVCTLPFRVYVYVYHKGIMLFGDFLCRLSTYALVNLCSIFEMTMSFFRCIAIVFPV 129
QY 129 RLHVTISRASAMILGIIWI-LIMASSIMLLDGSSENGSVTSCLEINLYKIAK--LQTM 185
DB 130 QNINLVTOKKARFVCVGIWIFVILITSSPFLMAKPKQDKGNNTKCEPPQDNQTKNHVVL 189
QY 186 NYIALVVGCLLPFTLSICVYLIIRVLKVEVBSGLRVSHRKALTTIITLIIFLCFL 245
DB 190 HVSLSFVGFIIFPVIIIVCYTMIITLLKSKMKN--LSHKKALGIMIVVTAFLVSFM 247
QY 246 PYHTLRVHLTTW--KVGICKD--RLHRAVLTTLAANAACPNFLVYPAGENFKORLK 301
DB 248 PYHIOHTIHLFHLNETKPCDSVLRMQKSVITLTLAASNCCEPDLTYFFSGGNFRKRL- 306
QY 302 SALRK 306
DB 307 STFRK 311

RESULT 4
US-08-153-848-44
; Sequence 44, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
```


TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-44

Query Match 28.0%; Score 479; DB 1; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY 7 FNNNSRNTTIE-NFKREFFPIVYLIIFFWGVLGNGLSIVFLQPKKSTSVVFMPLNLA 65
DB 15 FSLATAEQCGQETPEENMLFASFYLLDFILALVGNLTALMLFIRDHKSGTPANVFLMHLA 74
QY 66 ISDLLFISTLPFRADYLLRGSNMIFGDLACRIMSYSLYVNMYSIYFLTVLSVVRPLAMV 125
DB 75 VADLSCVLLPRLVLYHSGNMHPGEIACRLTGFLFLYLMYASIFYLTCISADRLALIV 134
QY 126 HPRLLHTYSIRSAWILGIIWILI-MASSIMLDGSGSNGSVTSCELENYKIAKLOT 184
DB 135 HPMKSLKRRPLVLAHACAFMLWVAVAPLVSPQVQTNHTVVCQ--LYR-EKASH 191
QY 165 MMYIALVGCCLRPFTLSICYLLIIRVLLKVEVPESGLRVSHR--KALTITITLTIIPF 241
DB 192 HALVSLAAVFTPTTITVTCYLLIIRSL-----RQGLRVEGRKLTKAVRMAIYVAIFL 245
QY 242 LCFELPYHTLRVTLTWTWKV--GLCKDRILKALV--ITTLAANAACFNPLLYYPAGENFK 297
DB 246 VCFVYVHVNRSVYVLYHSHGASCATQRIALANRITSCITSLNGALDPIIMYFVAEKPR 305
QY 298 DLKSAAL---RKGNPQAKTK 315
DB 306 HALCNILCGKRLKGPPSPSEK 327

RESULT 5
US-08-812-871-3
Sequence 3, Application US/08812871
Patent No. 5955303
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice

APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0237 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 992700
US-08-812-871-3

Query Match 28.0%; Score 479; DB 2; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY 7 FNNNSRNTTIE-NFKREFFPIVYLIIFFWGVLGNGLSIVFLQPKKSTSVVFMPLNLA 65
DB 15 FSLATAEQCGQETPEENMLFASFYLLDFILALVGNLTALMLFIRDHKSGTPANVFLMHLA 74
QY 66 ISDLLFISTLPFRADYLLRGSNMIFGDLACRIMSYSLYVNMYSIYFLTVLSVVRPLAMV 125
DB 75 VADLSCVLLPRLVLYHSGNMHPGEIACRLTGFLFLYLMYASIFYLTCISADRLALIV 134
QY 126 HPRLLHTYSIRSAWILGIIWILI-MASSIMLDGSGSNGSVTSCELENYKIAKLOT 184
DB 135 HPMKSLKRRPLVLAHACAFMLWVAVAPLVSPQVQTNHTVVCQ--LYR-EKASH 191
QY 165 MMYIALVGCCLRPFTLSICYLLIIRVLLKVEVPESGLRVSHR--KALTITITLTIIPF 241
DB 192 HALVSLAAVFTPTTITVTCYLLIIRSL-----RQGLRVEGRKLTKAVRMAIYVAIFL 245
QY 242 LCFELPYHTLRVTLTWTWKV--GLCKDRILKALV--ITTLAANAACFNPLLYYPAGENFK 297
DB 246 VCFVYVHVNRSVYVLYHSHGASCATQRIALANRITSCITSLNGALDPIIMYFVAEKPR 305
QY 298 DLKSAAL---RKGNPQAKTK 315
DB 306 HALCNILCGKRLKGPPSPSEK 327

RESULT 6
US-09-299-843A-44

```
Sequence 44, Application US/09239843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwaikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Bornun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Unl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-44

Query Match      28.0%; Score 479; DB 3; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY 7 FSNNSNRCTIEN-FKREFFPIVYLIIFWGVNGLSIYVLOPYKSTSVNFMNLIA 65
DB 15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLALMLFIRDKSGTPANVFMLHA 74
QY 66 ISDLFIETLPFRADYYLRGSMWIFGDLACRIMSYSLYVNNYSIYFLTVLSVRFAMV 125
DB 75 VADLSCVLVPRLVYHFGSNHMPFGELACRLTGFLFYLMNYASIFYLTCISADRFALIV 134
QY 126 HPFRLIHTSIRSAWILGIIWILI-MASSIMLDSGSEQNGSVTSCELANLYKIAKLOT 184
DB 135 HAVKSLKLRPLVYAHLCAPLWVAVAMAPLLVSPQTVQTNHTVCLQ--LYR-EKASH 191
QY 185 MNVIALVVGCLLPFTLSICYLLIRVLKVEVPSGLRVSHR---KALTTIITLIIFF 241
DB 192 HALVSLAVAFTEPFTITVYCYLLIIRSL-----RQGLRVEKRLTKAVRMALVLAIFL 245
QY 242 LCFPLPHITRLVHLTWKV--GLCKDRILKALV--ITLALAANAACENLLYYFAGENRK 297
DB 246 VCFVPHVNRSVYVLYHRSHGASCATQRIALANRITSCLTSLNGALDPIWYFVAEKPR 305
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```
QY 298 DRUKSL----RKGNPQKAKTK 315
DB 306 HALCNILCGKRLKGPSPFEGK 327

RESULT 7
US-09-088-337B-44
Sequence 44, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwaikart, Vicki L.
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Bornun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-JUN-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44

Query Match      28.0%; Score 479; DB 3; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY 7 FSNNSNRCTIEN-FKREFFPIVYLIIFWGVNGLSIYVLOPYKSTSVNFMNLIA 65
DB 15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLALMLFIRDKSGTPANVFMLHA 74
QY 66 ISDLFIETLPFRADYYLRGSMWIFGDLACRIMSYSLYVNNYSIYFLTVLSVRFAMV 125
DB 75 VADLSCVLVPRLVYHFGSNHMPFGELACRLTGFLFYLMNYASIFYLTCISADRFALIV 134
QY 126 HPFRLIHTSIRSAWILGIIWILI-MASSIMLDSGSEQNGSVTSCELANLYKIAKLOT 184
DB 135 HAVKSLKLRPLVYAHLCAPLWVAVAMAPLLVSPQTVQTNHTVCLQ--LYR-EKASH 191
QY 185 MNVIALVVGCLLPFTLSICYLLIRVLKVEVPSGLRVSHR---KALTTIITLIIFF 241
```

Db 192 HALVSLAFAFTEPFTTTCYLLIIRSL-----RQGLREVERKRLKTKAVRMIAIVLAIFL 245
 Qy 242 LCELPHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAANACFNPLVYFAGENRK 297
 Db 246 VCFVPHVNRSVYVHLHYRSHGASCATQRIILALANRITSCLTSLNGALDPIIMFVFAEKFR 305
 Qy 298 DRUKSAL----RKGNPOKAKTK 315
 Db 306 HALCNILCGKRLKGPPSPFEGK 327

RESULT 8

US-09-170-496D-32
 ; Sequence 32, Application US/09170496D
 ; Patent No. 6555339
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P.
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
 ; TITLE OF INVENTION: Receptor
 ; FILE REFERENCE: AREN-0040
 ; CURRENT APPLICATION NUMBER: US/09/170,496D
 ; CURRENT FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 294
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 32
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-170-496D-32

Query Match 28.0%; Score 479; DB 4; Length 339;

Best Local Similarity 34.8%; Pred. No. 1.2e-29; Mismatches 126; Indels 22; Gaps 9;

Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;
 Qy 7 PSNNNSRNCITEN-FKREFFPIVYLIFPMGVLGNGLSIVFLQPYKKSSTVVNFMPLNLA 65
 Db 15 FSLATREOCQGETPEENMLFASFYLLDFLALVGNLTALMLFTRDKSGTPANVFLMHLA 74
 Qy 66 ISDLFIISTLPFRADYLLRGSNMIFGDLACRIMSYSLVNMYSIYFLTVLSVREPLAMV 125
 Db 75 VADLSCVLLPFRLLVYHBSGNMHPFGEINCRLLGFLFLYINMVASIYFLTCISADRLALIV 134
 Qy 126 HPRRLHVTISRSAMILGIIWILI-MASSIMLDGSEQNSVTSCELENIYKAKLOT 184
 Db 135 HGVKSLKLRPLVYAHILACAFLLWVVAAPLVSPQVTQTNHTVCLQ--LYR-EKASH 191
 Qy 185 MNYIALVVGCLLPFTLSICYLLITRVLKVEPESGLRVSHR--KALTITITLIIFF 241
 Db 192 HALVSLAFAFTEPFTTTCYLLIIRSL-----RQGLREVERKRLKTKAVRMIAIVLAIFL 245
 Qy 242 LCELPHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAANACFNPLVYFAGENRK 297
 Db 246 VCFVPHVNRSVYVHLHYRSHGASCATQRIILALANRITSCLTSLNGALDPIIMFVFAEKFR 305
 Qy 298 DRUKSAL----RKGNPOKAKTK 315
 Db 306 HALCNILCGKRLKGPPSPFEGK 327

RESULT 9

PCT-US93-11153-44
 ; Sequence 44, Application PC/TUS9311153
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schmelkarc, Vicki L.
 ; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/11153
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448

TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
 PCT-US93-11153-44

Query Match

28.0%; Score 479; DB 5; Length 339;

Best Local Similarity 34.8%; Pred. No. 1.2e-29; Mismatches 126; Indels 22; Gaps 9;

Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;
 Qy 7 PSNNNSRNCITEN-FKREFFPIVYLIFPMGVLGNGLSIVFLQPYKKSSTVVNFMPLNLA 65
 Db 15 FSLATREOCQGETPEENMLFASFYLLDFLALVGNLTALMLFTRDKSGTPANVFLMHLA 74
 Qy 66 ISDLFIISTLPFRADYLLRGSNMIFGDLACRIMSYSLVNMYSIYFLTVLSVREPLAMV 125
 Db 75 VADLSCVLLPFRLLVYHBSGNMHPFGEINCRLLGFLFLYINMVASIYFLTCISADRLALIV 134
 Qy 126 HPRRLHVTISRSAMILGIIWILI-MASSIMLDGSEQNSVTSCELENIYKAKLOT 184
 Db 135 HGVKSLKLRPLVYAHILACAFLLWVVAAPLVSPQVTQTNHTVCLQ--LYR-EKASH 191
 Qy 185 MNYIALVVGCLLPFTLSICYLLITRVLKVEPESGLRVSHR--KALTITITLIIFF 241
 Db 192 HALVSLAFAFTEPFTTTCYLLIIRSL-----RQGLREVERKRLKTKAVRMIAIVLAIFL 245
 Qy 242 LCELPHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAANACFNPLVYFAGENRK 297
 Db 246 VCFVPHVNRSVYVHLHYRSHGASCATQRIILALANRITSCLTSLNGALDPIIMFVFAEKFR 305
 Qy 298 DRUKSAL----RKGNPOKAKTK 315
 Db 306 HALCNILCGKRLKGPPSPFEGK 327

RESULT 10

PCT-US95-07180-2
 ; Sequence 2, Application PC/TUS9507180
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, YI
 ; APPLICANT: GOCAYNE, JEANINE D
 ; APPLICANT: RUBEN, STEVEN M
 ; TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: CARBELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

```
/ ADDRESS: STEWART & OLSTEIN
/ STREET: 6 BECKER FARM ROAD
/ CITY: ROSELAND
/ STATE: NJ
/ COUNTRY: US
/ ZIP: 07068
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/07180
/ FILING DATE: 06-JUNE-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MULLINS, J.G.
/ REGISTRATION NUMBER: 30,073
/ REFERENCE/DOCKET NUMBER: 325800-366
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-994-1700
/ TELEFAX: 201-994-1744
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 339 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US95-07180-2
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Query Match 28.0%; Score 479; DB 5; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;
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QY 7 FSNMNRNCTIEN-FKREPPPIVYLIIFFWGVLGNGLSIVFLQPYKSTSVNVFMNLTA 65
DB 15 FSLATAEQCGQETPLNNMLFASFYLLDFILALVGNLTALMLFIRDKSGTPANVFLMHLA 74
QY 66 ISDLFIPTLPFRADYYLRGSMNWI FGDACRIMSISLYVMYSIYFLVLSVRFPLAMV 125
DB 75 VADLSCVLPFLPRLVYHFGSNMPPGEIACRLTGFLFLMWTASIFLTCISADRFALIV 134
QY 126 HPEFLHTVTSIRSAMILGIIWILI-MASSIMLLDSGSEONGSVTSCLEINLYKIATQ 184
DB 135 HPEVSLIKLRPLVYAHACAFLMWVAVAMAPILVSPQTQTNHTVVCLO--LYR-EKASH 191
QY 185 MNVIALVVGCLPFFFTLSICYLLIRVLKVEVPESGLRVSHR--KALTTIIITLIIFF 241
DB 192 HALVSLAVAFPTFPITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVMIAIVLAIPL 245
QY 242 LCFPLPYHTLRTVYLTWVKV--GLCKDRLHKALV--ITLALAANACFNPFLYYFAGEENK 297
DB 246 VCFVPHVNRSVYVLYHSHGASCATORILALANRITSLTSLNGALDPIWTFVAEKFR 305
QY 298 DRKSKAL---RKGHPOKAKTK 315
DB 306 HALCNMLCGKRLKGPSPFEKG 327
```

```
RESULT 11
US-09-170-496D-182
/ Sequence 182, Application US/09170496D
/ Patent No. 6555339
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
/ FILE REFERENCE: AREN-0040
/ CURRENT APPLICATION NUMBER: US/09/170,496D
/ FILING DATE: 1998-10-13
/ NUMBER OF SEQ ID NOS: 294
```

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/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 182
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-170-496D-182
```

```
Query Match 27.8%; Score 476; DB 4; Length 339;
Best Local Similarity 34.8%; Pred. No. 2e-29;
Matches 112; Conservative 61; Mismatches 127; Indels 22; Gaps 9;
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QY 7 FSNMNRNCTIEN-FKREPPPIVYLIIFFWGVLGNGLSIVFLQPYKSTSVNVFMNLTA 65
DB 15 FSLATAEQCGQETPLNNMLFASFYLLDFILALVGNLTALMLFIRDKSGTPANVFLMHLA 74
QY 66 ISDLFIPTLPFRADYYLRGSMNWI FGDACRIMSISLYVMYSIYFLVLSVRFPLAMV 125
DB 75 VADLSCVLPFLPRLVYHFGSNMPPGEIACRLTGFLFLMWTASIFLTCISADRFALIV 134
QY 126 HPEFLHTVTSIRSAMILGIIWILI-MASSIMLLDSGSEONGSVTSCLEINLYKIATQ 184
DB 135 HPEVSLIKLRPLVYAHACAFLMWVAVAMAPILVSPQTQTNHTVVCLO--LYR-EKASH 191
QY 185 MNVIALVVGCLPFFFTLSICYLLIRVLKVEVPESGLRVSHR--KALTTIIITLIIFF 241
DB 192 HALVSLAVAFPTFPITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVMIAIVLAIPL 245
QY 242 LCFPLPYHTLRTVYLTWVKV--GLCKDRLHKALV--ITLALAANACFNPFLYYFAGEENK 297
DB 246 VCFVPHVNRSVYVLYHSHGASCATORILALANRITSLTSLNGALDPIWTFVAEKFR 305
QY 298 DRKSKAL---RKGHPOKAKTK 315
DB 306 HALCNMLCGKRLKGPSPFEKG 327
```

```
RESULT 12
US-08-513-974B-374
/ Sequence 374, Application US/08513974B
/ Patent No. 6114139
/ GENERAL INFORMATION:
/ APPLICANT: Hinuma, Shuji
/ APPLICANT: Hosoya, Masaki
/ APPLICANT: Fujii, Ryo
/ APPLICANT: Ohtaki, Tetsuya
/ APPLICANT: Fukusumi, Shoji
/ TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
/ NUMBER OF SEQUENCES: 380
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
/ STREET: 130 Water Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/513,974B
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION NUMBER: PCT/JP95/01599
/ APPLICATION NUMBER: JP 7-093989
/ FILING DATE: 19-AUG-1995
/ PRIOR APPLICATION DATA:
```



```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-00-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-559-524A-4
```

Query Match 25.8%; Score 442; DB 2; Length 373;

Best Local Similarity 31.0%; Pred. No. 9.1e-27;

Matches 95; Conservative 78; Mismatches 109; Indels 24; Gaps 7;

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QY 16 TIENFKREPPPIYLLIFFWGVGLNGLSIVYFLQPKKSTSVNFMNLATISDLFIISTL 75
DB 45 TKTGFPYLLPAVYLLVIFLIGLNSVALIMFVFHMKPWSGISVNMENLALADFLVLT 104
QY 76 PFRADYLRGSMNIFGDLACRIMSYSLYVMYSSIVFLTVLSVRFLAMVHPRLHVT 135
DB 105 PALIFYFNKTDWIFGDAMCKLQRFIFHVNLYGSLIFLTCSAHRSGVVYPLSLGRLK 164
QY 136 IRSAMILCGIITWILMASSIML---DSGSQNGSVTSCLE-----LNLKYIAKLQTN 186
DB 165 KKNAYVISVLVWLIVVVGISPLIFYSGTGIRKNKTIIT-CYDTSDEYLSYSFYSMCT-- 221
QY 187 YIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIFLCPL 246
DB 222 --TVAMFC-VPLVLILGCTGLIVRALYKDLNSPLR---RKSIVYIIVLTVFAVSITP 275
QY 247 YHTLRVYHL-----TTWKVGLCKDRLHKAIVITLALAANAACPNPLIYPFAGENFKDRL 300
DB 276 FHWKTKMNLRARLDFOQPEMCAFNDRVYATYQVTRGLASLNSCVDPIIFYLAGDTPRRRL 335
QY 301 KSAIRK 306
DB 336 SRATRK 341
```

RESULT 15
US-08-749-707-4

Sequence 4, Application US/08/49707

Patent No. 6063582

GENERAL INFORMATION:

APPLICANT: Conley, Pamela B.

APPLICANT: Jantzen, Hans-Michael

TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP

STREET: 1800 M Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036-5869

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

```
APPLICATION NUMBER: US/08/749,707
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-01-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-707-4
```

Query Match 25.8%; Score 442; DB 3; Length 373;

Best Local Similarity 31.0%; Pred. No. 9.1e-27;

Matches 95; Conservative 78; Mismatches 109; Indels 24; Gaps 7;

```
QY 16 TIENFKREPPPIYLLIFFWGVGLNGLSIVYFLQPKKSTSVNFMNLATISDLFIISTL 75
DB 45 TKTGFPYLLPAVYLLVIFLIGLNSVALIMFVFHMKPWSGISVNMENLALADFLVLT 104
QY 76 PFRADYLRGSMNIFGDLACRIMSYSLYVMYSSIVFLTVLSVRFLAMVHPRLHVT 135
DB 105 PALIFYFNKTDWIFGDAMCKLQRFIFHVNLYGSLIFLTCSAHRSGVVYPLSLGRLK 164
QY 136 IRSAMILCGIITWILMASSIML---DSGSQNGSVTSCLE-----LNLKYIAKLQTN 186
DB 165 KKNAYVISVLVWLIVVVGISPLIFYSGTGIRKNKTIIT-CYDTSDEYLSYSFYSMCT-- 221
QY 187 YIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIFLCPL 246
DB 222 --TVAMFC-VPLVLILGCTGLIVRALYKDLNSPLR---RKSIVYIIVLTVFAVSITP 275
QY 247 YHTLRVYHL-----TTWKVGLCKDRLHKAIVITLALAANAACPNPLIYPFAGENFKDRL 300
DB 276 FHWKTKMNLRARLDFOQPEMCAFNDRVYATYQVTRGLASLNSCVDPIIFYLAGDTPRRRL 335
QY 301 KSAIRK 306
DB 336 SRATRK 341
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Search completed: March 18, 2005, 16:22:31
Job time : 32.7544 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2005, 16:09:33 ; Search time 25.8728 Seconds
(without alignments)
1227.218 Million cell updates/sec

Title: US-09-826-791A-2

Perfect score: 1712
Sequence: 1 MEKNGTFENNNSRNCTIENF.....KAKTKCFPVSVWLAKITRV 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	467	27.3	362	2	S33733 G protein-coupled
2	447	26.1	308	2	I50241 G protein-coupled
3	446	26.1	373	2	JC4737 G protein-coupled
4	442	25.8	373	2	JC4162 P2Y receptor - bov
5	440	25.7	361	2	B45680 G protein-coupled
6	436	25.5	344	2	T09508 Intron 17 purinerg
7	430	25.1	370	2	JC5549 heptahelical p2y5-
8	418.5	24.4	373	2	A47556 ATP receptor p2u -
9	416	24.3	342	2	S13638 platelet-activatin
10	416	24.3	375	2	A54946 P-2U nucleotide re
11	409.5	23.9	342	2	A40191 platelet-activatin
12	404.5	23.6	420	2	I51667 thrombin receptor
13	404	23.6	341	2	S63666 platelet activatin
14	400.5	23.4	397	2	S66518 proteinase-activat
15	398	23.2	380	2	I38435 angiotensin recept
16	397	23.2	341	2	S43252 platelet-activatin
17	394.5	23.0	355	2	A45177 chemokine (C-C) re
18	391	22.8	328	2	I55450 G protein-coupled
19	390.5	22.8	355	2	I49339 macrophage inflamm
20	390	22.8	399	2	I48705 proteinase activat
21	387	22.6	371	2	JC5796 probable chemattr
22	382	22.3	371	2	JC5498 G protein-coupled
23	378.5	22.1	378	2	B55735 lymphocyte-specifi
24	378	22.1	355	2	JC5067 G protein-coupled
25	376	22.0	356	2	I49340 MIP-1 alpha recept
26	373.5	21.8	387	2	I69202 G protein-coupled
27	372.5	21.8	363	2	I57955 somatostatin recep
28	372.5	21.8	364	2	JN0763 somatostatin recep
29	372.5	21.8	378	2	A55735 G protein-coupled

30	372	21.7	363	2	I57940 somatostatin recep
31	371.5	21.7	365	2	S68208 G protein-coupled
32	370.5	21.6	383	2	S85594 G protein-coupled
33	370	21.6	365	2	S68679 G protein-coupled
34	366	21.4	355	2	G02436 chemokine (C-C) re
35	366	21.4	427	2	S17148 alpha-thrombin rec
36	364.5	21.3	362	2	JN0694 angiotensin II rec
37	363	21.2	359	2	S15403 angiotensin II rec
38	361.5	21.1	352	2	A43113 chemokine (C-C) re
39	360	21.0	432	2	A43448 thrombin receptor
40	357	20.9	328	2	JC4800 P2Y6 receptor - hu
41	356.5	20.8	333	2	I65989 G protein-coupled
42	356.5	20.8	361	2	JC5653 G protein-coupled
43	356.5	20.8	378	2	A45680 G protein-coupled
44	356	20.8	359	2	A48857 angiotensin II rec
45	356	20.8	363	2	A49092 angiotensin II rec

ALIGNMENTS

```
RESULT 1
S33733
G protein-coupled receptor - chicken
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S33733
R/ webd, T.E.; Simon, J.; Kriehak, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock
FEBS Lett. 324, 219-225, 1993
A/Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A/Reference number: S33733; MUID:93285340; PMID:8508924
A/Accession: S33733
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-362 <MEB>
A/Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CA51716.1; PID:g395084
C/Superfamily: ATP receptor p2u
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match      27.3% ; Score 467; DB 2; Length 362;
Best Local Similarity 30.7% ; Pred. No. 8, 7e-31;
Matches 98; Conservative 83; Mismatches 112; Indels 26; Gaps 7;

QY 5 GTFSSNNNSRNCTI--ENKREKRPPIVYLIIFFWGVGLSGLSIYVLPQIPYKSTSVNVFPL 62
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 21 GWAGNATTKCSLITRTGQFYFLPTVYIIVFITGFLGNSVAIWMVFHMRPWSGISVNF 80
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 NLAISDLLPISTLPFRADYLRGNSMIFGDLACRIHSYSLYVNMYSIYFLTVLSVVRFL 122
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 81 NLALADFLVLTLPALIFRYENKTDWIFEDVWCKLQRFIFVNLVGSILFLICISVHRYT 140
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 AMVHPFRLIHTVSIRSANILGIIWILIMASSIMDL--DSGSEONGSVTSCLE----- 173
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 141 GVVHFLKSLGRKKNAVYVSSLVVALVAVIAPILFPGSGTVRRNKKIT-CYDTADDEX 199
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 LNLVYIAKLQTMNYIALVVGCLLPFTLSICYLIIIRVLIAKVEVSGRVRHRAKLTIT 233
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 200 LRSYFVYSWCTTVFMFCI----PPIVILGCGGLIVKVLIVDLDLNSPLR---RSKIYIV 251
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 224 IITLLIIFLCPLPYHTLRTFVHL-----TWVVGICOKRIHKAIVTTLAANACFNPFL 287
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 252 IIVLTVFAYSVLPFVWMTKLNLNRLADPOTPOWCAFNDRKVAITYOVTKGLASNSCVDP 311
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 288 LYYFAGENFKDRLKSLAKR 306
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 312 LYFLAGDTFRRRLSRATRK 330
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
I50241
G protein-coupled receptor 6H1 - chicken
N/Alternate names: purinoceptor 6H1
C/Species: Gallus gallus (chicken)
```

R: Ayyathan, K.; Webb, T.E.; Sandhu, A.K.; Althwal, R.S.; Barnard, E.A.; Kunepuli, S.P. Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A: Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.

A: Reference number: J04615; M01D:96158962; PMID:8579591

A: Accession: J04615

A: Molecule type: mRNA

A: Residues: 1-373 <ANY>

A: Cross-references: GB:U4029; NID:91147730; PIDN:AAA97872.1; PID:g1147731

A: Experimental source: erythro leukemia cells

R: Leon, C.; Vial, C.; Cazeneuve, J.; Gachet, C.

A: Submitted to the EMBL Data Library, May 1995.

A: Description: Cloning of a human putative P2Y receptor.

A: Reference number: S54253

A: Accession: S54253

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 1-137, 139-373 <IRED>

A: Cross-references: EMBL:249205; NID:979835; PIDN:CAA9066.1; PID:g798836

C: Comment: This receptor belongs to a family of G protein-coupled receptors. It responds

C: Genetics:

A: Gene: P2Y1; GDB:P2RY1

A: Cross-references: GDB:677125; OMIM:601167

A: Map position: 3pter-3pter

C: Superfamily: ATP receptor P2U

C: Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F: 52-77/Domain: transmembrane #status predicted <TM1>

F: 88-111/Domain: transmembrane #status predicted <TM2>

F: 124-153/Domain: transmembrane #status predicted <TM3>

F: 171-191/Domain: transmembrane #status predicted <TM4>

F: 214-233/Domain: transmembrane #status predicted <TM5>

F: 261-282/Domain: transmembrane #status predicted <TM6>

F: 305-328/Domain: transmembrane #status predicted <TM7>

F: 327-373/Binding site: phosphate (Ser) (covalent) #status predicted

F: 258-336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predict

F: 330-333/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict

F: 343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-depend

Query Match 26.1%; Score 446; DB 2; Length 373;

Best local similarity 32.1%; Pred. No. 4.6e-29;

Matches 102; Conservative 79; Mismatches 111; Indels 26; Gaps 10;

QY 6 TESNNNSRNC--TLENKREFFPIYVLIIFPFGVLNGSLIVFLQPYKSTSVNFMLN 63

DB 33 TAAVSSFFKCALFKTGQFYLLPAVYLVIIIFGLNLSVALIMFVPMKPMWSISYVMN 92

QY 64 LAISDLFIETLPPRAYLYRGSNMIFGLDACKIMSYSLVMNYSIYELTVLSVRFPLA 123

DB 93 LALDPLFYVLLPLLIIFYYNKTDWIFGDAMCKLQRFPHVMLYGSLFLTCISAHRYSG 152

QY 124 MVHDFRLAHTYSIRSAMIIIGLIW-ILIMASSIMLDSSG--EONSVSQLE-----L 174

DB 153 VVYVFLKSLGRLKKKNAICISLVMLVVALISPIILFYSGTGVRKAKTII-CYDTTSDEL 211

QY 175 NLKYIACLGQNMNVIYLVGCLPFFFLISICYLIIIVLILKVEPESGLRVSHRKALTTI 234

DB 212 RSYFIYSMCT---TVAMFC-VPLVLIIDGCGYIALYIKDLNSPLR---RKSIIYVI 263

QY 235 ITIILIFELCPLPHYTRVHLLT---MKVGC--KDRILKALVITLILAAANACFNPL 288

DB 264 IVLTIVFVSVIIFPHWKNMLRAKLDFTPRMCAFRNDVYATVYQVTRGLASINSCVDPL 323

QY 289 YTFAGENFKDRLSALRK 306

DB 324 YPLAGDTFRRRLSRATRK 341

RESULT 4

J04162

P2Y receptor - bovine

C: Species: Bos primigenius taurus (cattle)

C: Date: 12-Oct-1995 #sequence _revision 10-Nov-1995 #text _change 09-Jul-2004

C: Accession: J04162

C: Henderson, D.U.; Elliott, D.G.; Smith, G.M.; Webb, T.R.; Dairty, T.A.

Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A>Title: Cloning and characterization of a bovine P2Y receptor.
A|Reference number: J04162; MUID:95352058; PMID:7626079
A|Molecule type: mRNA
A|Rosetta: 1-373 <HNP>
A|Cross-references: UNIPROT:P48042; EMBL:X87628; NID:g1032484; PIDN:CMA60958.1; PID:g103
A|Experimental source: bovine endothelial cell
C|Genetics:
A|Gene: bomp2y
C|Superfamily: ATP receptor P2U
C|Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
P:52-77/Domain: transmembrane #status predicted <TM1>
P:88-111/Domain: transmembrane #status predicted <TM2>
P:124-150/Domain: transmembrane #status predicted <TM3>
P:171-191/Domain: transmembrane #status predicted <TM4>
P:214-237/Domain: transmembrane #status predicted <TM5>
P:261-282/Domain: transmembrane #status predicted <TM6>
P:305-328/Domain: transmembrane #status predicted <TM7>
P:111,27,113,197/Binding site: carbohydrate (asn) (covalent) #status predicted
P:158/Binding site: phosphate (ser) (covalent) (by protein kinase A) #status predicted

Query Match 25.8%; Score 442; DB 2; Length 373;
Best Local Similarity 31.0%; Pred. No. 9,8e-29;
Matches 95; Conservative 76; Mismatches 109; Indels 24; Gaps 7;

Gy 16 TLENPRKEFPPIVYLIIFFWGLNGLSIVFLDPYKSTSVNVFMLNAISDLLFIITL 75
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 45 TKTFQPPYYLPAYVILIFIGFLGNSVAIMWFVFPMKEMSGISVYMFLADFLVLT 104
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Gy 76 PRADYYLAGSNMIFGDLACRIMSLSLVNNYSSTYFTLVSVAFPLAVHFRLLHTVS 135
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 105 PALIFFYFNKTWDIFGMCKLORFIFPVNLVGSILFTICISAHRSYGVAVPDKSLGRUK 164
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Gy 136 ISAWMLIGIIVTILIMASSIMTL---DSGEONGSVTSCLD-----INLYIKLKQTNN 186
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 165 KKNNAVVISLVNMLIVVGISPILEFGSGTGIRKKNTIT-CYDTSDSEYLRSTYISKCT-- 221
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Gy 187 YZALVVGCLPFPTLSICYLLIRVLKVEVESGLRVSHRKALTITITITLIFPLCFRP 246
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 222 --TVANFC-VPLVLIGCYGVIALITYKOLDNSLR---KSIYLVITIVLVANSYTP 275
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Gy 247 YHTLRFTVHL-----TTKVGLCKDRLHKALVTITALAANAQENPLLYFAGENFKRL 300
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 276 FYVMKMTMNLRARLDPEPCMCAPENDRYATYQVTRGLASLNSCVDPIYFLAGDFERRRL 335
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Gy 301 KSALKR 306
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 336 SRATRK 341
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 5
B45680
G protein-coupled peptide receptor EBI 2 - human
C|Species: Homo sapiens (man)
C|Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C|Accession: B45680
R|Bitenbach, M.; Josefsen, K.; Valamanchili, R.; Lenolt, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A|Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled P
A|Reference number: A45680; MUID:93186173; PMID:838238
A|Accession: B45680
A|Status: preliminary
A|Molecule type: nucleic acid
A|Residues: 1-361 <BIR>
A|Cross-references: UNIPROT:P32249; GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057
A|Experimental source: B-lymphocytes
A|Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBIID:127097)
C|Superfamily: ATP receptor P2U
C|Keywords: G protein-coupled receptor; transmembrane protein

Query Match 25.7%; Score 440; DB 2; Length 361;
Best Local Similarity 32.1%; Pred. No. 1,4e-28;

[illegible]

C:\Species: Homo sapiens (man)
C:\Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
C:\Accession: A54946
R:\Part, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Hurch, L.H.; Olsen, J.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994
A:\Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic
A:\Reference number: A54946; MUID:94211846; PMID:8159738
A:\Accession: A54946
A:\Status: preliminary
A:\Molecule type: mRNA, protein
A:\Residues: 1-375 <PAR>
A:\Cross-references: GB:U07225
A:\Note: parts of this sequence were confirmed by protein sequencing
C:\Genetics:
A:\Gene: GDB:P2RY2; HP2U; P2U
A:\Cross-references: GDB:362713; OMIM:600041
A:\Map position: 11q13.5-11q14.1
C:\Superfamily: ATP receptor P2U
C:\Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.3%; Score 416; DB 2; Length 375;
Best Local Similarity 31.6%; Pred. No. 1,3e-26;
Matches 100; Conservative 67; Mismatches 131; Indels 18; Gaps 8;

QY 4 NGTSSNN-SKNCTI-ENFKREFPIYVLIIFNGVLGNGSLVFLQPYKSTSVNVM 61
DB 13 NGTMDGDELGRCFENEDPKYVLLPVSYGVCCVGLCLINAVGLYIFLCRLITWNASTTYM 72
QY 62 LNLAIISDLFLSTLPFRADYVLRGSNNWIFGDLARINSYSLYVMYSSYVFLTSLVRF 121
DB 73 FLHNSDLVYASLPLVLYYARGDHPFSTVLCVAFVFLTYMDYCSILPLTCSVHRC 132
QY 122 LAMVHPEFLHVTSTIRSAMILCGIIMVIMASSIMLDSGSEONGSVTSCHELNLYXIAK 181
DB 133 LGVLRPLRSLMNGRABRVAVAGAVWVLVLCQAPVLVFTVTSRGPITCHDTSAPELFS 192
QY 182 LQTMNYALVYGL-LPEFTLSICYLLIIVLKEVPS-GLRVSHKALTTITITLI 238
DB 193 -RPAVSSVVMGLFLFAVFAVILVCCVLMARLLKPAVGTSGGLPRAKKSVRTIAVLA 251
QY 239 IEPFLCELPYHLRLVHLITMKVGLCKORLHKAIVTLA-----LAAANACNPLLYFAG 293
DB 252 VFALCELPFHVTRKLYYSFSLDL--SCHTLNAINNAVYKTVRLASANSCLDPVLYFLAG 308
QY 294 ENFKRRLKSLARKGHP 309
DB 309 Q----RLVFRPADKP 320

RESULT 11
A40191
A:\Species: Homo sapiens (man)
C:\Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
C:\Accession: A40191; JH0479; A41079; JCI359; A42831; IS1923
R:\Part, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A:\Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell sur-
A:\Reference number: A40191; MUID:92250505; PMID:1374385
A:\Accession: A40191
A:\Molecule type: mRNA
A:\Residues: 1-342 <KUN>
A:\Cross-references: UNIPROT:P25105; GB:M76674; NID:9456293; PIDN:AAA60002.1; PID:945629
R:\Part, R.D.; Prosenitz, E.R.; Zou, A.; Cochran, C.G.
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A:\Title: Characterization of a human cDNA that encodes a functional receptor for platelet-
A:\Reference number: JH0479; MUID:92028922; PMID:1656963
A:\Accession: JH0479
A:\Molecule type: mRNA
A:\Residues: 1-342 <YBR>
A:\Cross-references: GB:M00436; NID:g189537; PIDN:AAA60001.1; PID:g189538
A:\Experimental source: granulocyte, cell line HU-60 all
R:\Name, M.; Honda, Z.; Izumi, T.; Sakane, C.; Mutoh, H.; Minami, M.; Ito, H.; Sey

J. Biol. Chem. 266, 20400-20405, 1991

A>Title: Molecular cloning and expression of platelet-activating factor receptor from hu
A.Reference number: A41079; MUID:92041873; PMID:1657923

A.Accession: A41079

A>Status: not compared with conceptual translation

A.Molecule type: mRNA

A.Residues: 1-342 <NAK>

A.Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BA01050.1, PID:g219976

R.Susimoto, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mucho, H.; Shimizu, T.; Kurachi, Y.

Biochim. Biophys. Res. Commun. 189, 617-624, 1992

A>Title: Molecular cloning and characterization of the platelet-activating factor recept
A.Reference number: JCI359; MUID:93112021; PMID:1281995

A.Accession: JCI359

A.Molecule type: mRNA

A.Residues: 1-315,'N',317-342 <SUG>

A.Experimental source: heart

A>Note: The authors translated the codon AAT for residue 316 as Lys

R.Seifried, C.E.; Schweickart, V.L.; Godtke, R.; Gray, P.W.

Gemotoc 13, 833-834, 1992

A>Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns

A.Reference number: A42831; MUID:92347886; PMID:1322356

A.Accession: A42831

A.Molecule type: DNA

A.Residues: 1-226,'TG',229-342 <SEY>

A.Cross-references: GB:M8177; NID:g190697; PIDN:AAA6214.1, PID:g190698

A.Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIPI:109814)

R.Chase, P.B.; Halonen, M.; Regan, J.W.

Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

A>Title: Cloning of a human platelet-activating factor receptor gene: evidence for an in
A.Reference number: I51923; MUID:93192035; PMID:8383507

A.Accession: I51923

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-342 <RES>

A.Cross-references: GB:I556396; NID:g298580; PIDN:AAB25755.1; PID:g298581

C.Genetics:

A.Gene: GDB:PTAFR

A.Cross-references: GDB:128806; OMIM:173393

A.Map position: 1p35-1p34.3

C.Superfamily: ATP receptor P2U

C.Keywords: G protein-coupled receptor; transmembrane protein

F.I17-38/Domain: transmembrane #status predicted <TRI>
F.92-75/Domain: transmembrane #status predicted <TII>
F.92-113/Domain: transmembrane #status predicted <TRV>
F.134-155/Domain: transmembrane #status predicted <TRV>
F.184-205/Domain: transmembrane #status predicted <TVI>
F.233-253/Domain: transmembrane #status predicted <TVI>
F.277-297/Domain: transmembrane #status predicted <VII>

Query Match 23.9%; Score 409.5; DB 2; Length 342;
Best Local Similarity 31.3%; Pred. No. 4.1e-26;
Matches 103; Conservative 64; Mismatches 137; Indels 25; Gaps 9;

Dy 1 MEPNSTFSNNNSRNCTTENFKKEFPPIVYLIFFGVGLNGSLTYF--LQPYKKSISVN 58
 :
Dy 1 MEPHDS-SHMDS-----EFRTPLPFIYSIIFVLGVANGVYLMFARLTPCKFEIK 53
 :
Dy 59 VFMLALASDLFLISTPRADYYLRGSNWIPGDLACRINSYSLYNMYSITPLTVLSV 118
 :
Dy 54 IFMVNLTMADMFLFTLLPLMIYVYNOGNWILPKPLCNVAGCLFFINTYCSVAFLGVITY 113
 :
Dy 119 VFLLMVFHPRLIHVTSIRSAMLGCIILWLIM--ASSIMLDS-----GSEONGSVTSC 171
 :
Dy 114 NRFOAVTRIKRAQNTRKRGISLSLIWIWAIYGAA SYFILDSNTVPDSAGSGNVTRC 173
 :
Dy 172 LEMLNYKIAKLTQMYNIYALVGGCLRPFTLSICYLLIRLVLYKVEPSGLRVSHRKALT 231
 :
Dy 174 FE-HYEKGSGVPALIIHFIVSFELVFLILLFCNLVIRFLTLMQPVQQORNAEVRRALM 232
 :
Dy 232 TIITLIIIFLCFLPHLTRVHTLTKWKVGLCDRLHKAL----VTLLALAANAACFRPL 287
 :
Dy 233 MCVTLAVAFITICFVPHHVQ-LFWTLAEIGFQDSKFDQAINDAHQVTLCLSTNCULDPV 291

```

QY      288  LYYFAGENFKDRLKSLARKGHPQAKTKC 316
          :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      292  IYCFLLTKKFR--KHLTEKFYSMSSRRC 317

```

RESULT 12

I:151667
 thrombin receptor - African clawed frog
 C:Species: *Xenopus laevis* (African clawed frog)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: I51667
 R:Gerszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevich, T.; Turck, C.W.; Vu, T.H.; C
 Nature 368, 648-651, 1994
 A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac
 A:Reference number: I51667; MUID:94195429; PMID:8145852
 A:Accession: I51667
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-420 <GB>
 A:Cross-references: UNIPROT:P47749; EMBL:U09632; NID:g495197; PIDN:AAA18498.1; PID:g4951

Query Match	32.6%	Score 404.5	DB 2	Length 420
Best Local Similarity	23.4%	Pred. No. 1.3e-25		
Matches 99, Conservative	61	Mismatches 123	Indels 23	Gaps 6

```

QY 13 RNCITIE-----NFKREFFPIVYLIIFPMWGLANGSLIYELDOPKYSTSVNFMNTLA 65
Db 85 RNTTKAEQYLSQOMITKTFPESLYIVVFIYGLPMLNLAIIIFLRKTKRKAUVYMLNLA 144
QY 66 ISDLFI STLPRPADYYLNGSNWIFGDLACRIMSYSLYNNYSSIFYLTVLSVRFIAMY 125
Db 145 IADVFVSVALPFRIATHSLGNDMLGPGMCRIVTIFPCNNYCGVLLIASISYDRFIAYV 204
QY 126 HPERLIATHSIRSAMWLCGIWILIMASSIMLDGSEQ--NGSVTSCLEINLYKIAKL 182
Db 205 YPHNSLSMWTBKAAYACSFIMLISASTIPLVTEQOQKIPRIDITTCHEVDLDRKLD 264
QY 183 QIMNYIALVAGCLL---PFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTIITTL 238
Db 265 FYIYYVSSR--CLLFFFPVPIITTYICIGIIRLSSSSIENS---CKKTALFLAAVVL 319
QY 239 IFELCELPYHTLRTVYLITTWKVGCLCKDRJHKLVTTLTAAANCFMPLLYIFPAGENFKD 298
Db 320 VFILICGPIINVLFLTHY----LQANEPFLRYIILISACVGSVSCDPLIITYANSSQCR 375

```

QY	299	RLKSAL	304
Db	376	YLYSL	381

RESULT 13

S63666
platelet activating factor receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S63666
R:Shih, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.
Biochem. J. 314, 671-678, 1996
A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localization, and expression
A:Reference: S63666; MUID:96235129; PMID:8670084
A:Accession: S63666
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-341 <ISH>
A:Cross-references: UNIPROT:Q62035; EMBL:D50872; NID:g1256924; PIDD:BAA09468.1; PTD:g1256924
A:Superfamily: ATP receptor P2u

```

Query Match      23.6%; Score 404; DB 2; Length 341;
Best Local Similarity 30.5%; Pred. No. 1.le-25;
Matches 101; Conservative 66; Mismatches 134; Indels 30; Gaps 10;

OY      1 MERNGTSSNNNSRNCCTENFKREPPPIYLLIFFGVGNGLSLVFF--LQPYKKSSTSVN 58
||| ||| : : : ||||| : ||| : ||| : ||| :

```

```

D0 1 MENGSFRVDS-----EFRYTLPEIYVSIFILGVAAVGYLWVPAFNIYPSKQLEIK 53
QY 59 VPMNLAIADLLFISTLPPRADYYLRGNSMIFGLDACIMSYSLXYMMYSIVETLTVSY 118
D0 54 IFVNLITMADLLFLLTLPMTIYYVYNGEDMTLPNFCVAGACLEFFINYSVAPLGVITY 113
QY 119 VRELVAHPRLRLHYTSIRSAWILCGIIMILMMSIMTLDGSG-----EONGSVTSC 171
D0 114 NRQVAVAYIKTAQOTTRRGISLILTIWVSIVATASYFLATDSTNLPVNNDSGNTTRC 173
QY 172 LE-LNLYKAKIQTMNVIALVYGC-LIEFFLSTCYLLIIRVILKVEVPESGLRVSHRKA 229
D0 174 FEHYEYVSPIILVHVAFINL---CFELVFFELFPCNLVIITLTLTOPKROQRKAGVGRKA 230
QY 230 LTTIITITLLIIFELCELPYHTLETVAHLTTMKVGLCKDRILAKL-----VITLALAANAFCN 285
D0 231 LMMVCTVLAVFIFICEVPHVVO-LPWTILAEIGY-QTMVHQIMDAHOITLCLSTNCULD 288
QY 286 PLILYVAGENFKDRLKSALRKGHPOKATKC 316
D0 289 PVLYCFLTKKFKKHL---EKFYMSRSRKC 316

```

RESULT 14

proteinase-activated receptor 2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text_change 03-Jul-2004
C:Accession: S66518; S64709; G02131
C:NYSredt, S.; Emilsson, K.; Larsson, A.K.; Strombeck, B.; Sundelin, J.
Eur. J. Biochem. 232, 84-89, 1995
A>Title: Molecular cloning and functional expression of the gene encoding the human protease-activated receptor 2
A:Reference number: S66518; NCBI:96048032; PMID:7556175
A:Accession: S66518
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <YVS>
A:Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:g1008084; PIDN:CAA90290.1; PID:g1006
R:Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn, M.L.; Coughlin, S.R.
Biochem. J. 314, 1009-1016, 1996
A>Title: Molecular cloning, expression and potential functions of the human proteinase-activated receptor 2
A:Reference number: S64709; NCBI:96177879; PMID:8615752
A:Accession: S64709
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137, 'A', 139-397 <BOE>
A:Cross-references: EMBL:U34038; NID:g1041728; PIDN:AA87871.1; PID:g1041729
A>Note: the authors translated the codon GTC for residue 68 as Ile and AAC for residue 2
R:Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
;Reference number: H00822

Query Match	23.4%	Score 400.5	DB 2	Length 397
Similarity	30.7%	Pred. No. 2.6e-25		
Best Local				
Matches 99	Conservative	69	Mismatches 121	Indels 33
				Gaps 9

Oy 84 RGSNNI FGD LACRIMSYSLVYNNMYSII FLTVLSVRFLAVHDFRLHTVSIRSAWILC 143
Dd

```

Db      137 HGNMNYGALCNVLIGFFYGMNYSILFMTCLSVGRVWVIVNPMG----HSRKANTAI 192
Qy      144 GI---IWIIMASSIML-----LDSGSEONGSVTSCLEMLYKIAKLQTMNY-I 188
Db      193 GISLAIMLLILVITIPLYVVKOTIFIPAL-----NITTCGDVLPBQLVGDMMENYFL 244
Qy      189 ALVGC-LLPFTLSICYLIIIRVLKVEVPESGLRVSHRKALTTIITL..IFLCFLPY 247
Db      245 SLAIGFPLPAPFLTSAVYVLMIRLSSAMDENSEK-KRKRAIKLIVTVMYVLICTPS 303
Qy      248 HTLRVHLTTMWGKCKDRLHKALVITTLAAANACFNPPLYFAGENFKDRLKSALRK 307
Db      304 NLLLVHVFYLRK-SGGQSHVVALYIVALCLSTLNSCIDPPVYTFVSHDPRDIHAKNAL-- 360
Qy      308 HQKAKTKCVFPVSVWLKRETR 329
Db      361 -CRSVRTVKQMOMVSLTSKGR 381

```

RESULT 15

138435

angiotensin receptor homolog APJ - human

C:Species: Homo sapiens (man)

C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 03-Jul-2004

C:Accession: I38435

R.O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr

Gene 136, 355-360, 1993

A>Title: A human gene that shows identity with the gene encoding the angiotensin receptc

A:Reference number: I38435; MUID:94124031; PMID:8294032

A:Accession: I38435

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-360 <RES>

A:Cross-references: UNIPROT:P35414; EMBL:U03642; NID:G425351; PIDN:AAA18954.1; PID:G4253

C:Genetics:

A:Gene: APJ

A:Map position: 11q12

A:Introns: #status absent

C:Superfamily: vertebrate rhodopsin

Query Match 23.2%; Score 398; DB 2; Length 380;

Best Local Similarity 29.2%; Pred. No. 3.9e-25;

Matches 100; Conservative 71; Mismatches 134; Indels 38; Gaps 13;

```

Qy      1 MEPNGTFSN---NNSRNCTIENFKRE--FPPIVYLIIFFWGLGNGLSIY-VFLQPYRK 53
Db      1 MEEGGDFDNYGADNQSECEYTDWKSSGALIPALVMLVFLGTGNGLVLTWVPRSSREX 60
Qy      54 STSVNVFMNLAIISDLFIPTPRADYYLRGSNWIFGDLACRIMSISLYVNMYSIYFL 113
Db      61 RRSADIPIASLAVADLTFTVTLPLMATYTYRDYDWFPGTFCKLSYLLIFVMYASVFL 120
Qy      114 TVLSVVRFLAMVHPFLHVTGIRSAMILCGIIML--IMASSIML--DSGSEONGSVTS 170
Db      121 TGLSFDRIYLAIRPVANARLRVSCAVATAVLAWLALAMPVWLRTTGLENTTKVQ 180
Qy      171 CLEMLYKIAKLQ-----MNYIALVVGCLLPFTLSICYLIIIRVL-----KVEV 217
Db      181 CY-MDYSMVATVSEWAMEVGLGVSSTYGVFPFTIMLTCTYFFIAQTIGHFRKERIE- 238
Qy      218 PESGLRVSHRKALTTIITLIIIFLCFLDYHTLRVH---LTTWKVGLCKDRLHKALVI 273
Db      239 ---GLR-KRRRLISIVLVVTFALCMPEYHLVKTLYMGLSLHWP---CDFDLFLMNIF 291
Qy      274 --TLALAANACFNPPLYFAGENFKDRLKSALRKHPQAKT 314
Db      292 PYCTCISYVNSCLNPLIYAFDPRFRQACTSMLCGSGSRAGT 334

```

Search completed: March 18, 2005, 16:21:22

Job time : 27.8728 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 19:51:04 ; Search time 3868.5 Seconds
(without alignments)
9770.662 Million cell updates/sec

Title: US-09-826-791A-1

Perfect score: 993
Sequence: 1 atggaaccaaatgacaccc.....gaaaggaacaagagataaa 993

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_eef1:*
2: gb_eef2:*
3: gb_hic:*
4: gb_eef3:*
5: gb_eef4:*
6: gb_eef5:*
7: gb_eef6:*
8: gb_g8a1:*
9: gb_g8a2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	693	69.8	720	7	CO959137
2	675	68.0	758	6	CD630086
3	666	67.1	762	6	CD630084
4	663	66.8	745	6	CD630072
5	661.2	66.6	726	6	CD630089
6	632	63.6	753	6	CD630075
7	619.2	62.4	750	6	CD630077
8	618	62.2	673	6	CD630069
9	607.2	61.1	729	7	CO959148
10	603	60.7	652	6	CD630079
11	599.4	60.4	670	6	CD630087
12	596.8	60.1	663	6	CD630081
13	593.4	59.8	682	6	CD630067
14	565	56.9	729	7	CF147785
15	543	54.7	633	6	CD630066
16	540.8	54.5	621	6	CD630074
17	539.6	54.3	1739	3	AK008997
18	521	52.5	844	6	CD630082
19	515.6	51.9	860	6	CD630070
20	505	50.9	848	6	CD630090
21	478.8	48.2	827	6	CD630073
22	470.8	47.4	798	6	CD630076
23	463	46.6	808	6	CD630088
c 24	457.8	46.1	809	6	CD630068

25	439.6	44.3	1015	6	BY754684	BY754684
c 26	428	43.1	763	6	CD630078	CD630078
c 27	414.4	41.7	740	6	CD630080	CD630080
c 28	412	41.5	735	6	CD630085	CD630085
c 29	404.6	40.7	812	6	CD630071	CD630071
c 30	404.4	40.7	620	4	BI961697	BI961697
31	339.2	34.2	605	4	BI960974	BI960974
c 32	333	33.5	656	6	CD630083	CD630083
c 33	301.2	30.3	319	8	AQ001459	AQ001459
c 34	179.4	18.1	604	1	AI178926	AI178926
c 35	169.2	17.0	476	5	BX481095	BX481095
c 36	146.8	14.8	996	9	CL092116	CL092116
c 37	143.2	14.4	2755	3	AK033476	AK033476
38	125	12.6	833	7	CO919341	CO919341
39	123.4	12.4	842	7	CN503141	CN503141
40	123.4	12.4	870	7	CO929273	CO929273
41	121	12.2	720	7	CF147786	CF147786
42	120.4	12.1	666	8	BZ214361	BZ214361
43	116.8	11.8	538	7	CV030948	CV030948
44	116.4	11.7	671	6	CA376521	CA376521
45	114	11.5	1352	3	CR67452	CR67452

ALIGNMENTS

RESULT 1
CO959137/c
LOCUS
DEFINITION
AGENCOURT 30842218 NIH MGC 146 Homo sapiens cDNA clone
IMAGE:7389737 3', mRNA sequence.

ACCESSION
CO959137
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgs.nci.nih.gov/.
1 (bases 1 to 720)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contract: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga9bs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRB7 row: f column: 03
High quality sequence start: 20
High quality sequence stop: 632.
Location/Qualifiers

FEATURES

source
1..720
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7389737"
/feature_type="mixed"
/lab_host="NIH MGC 146"
/clone_1lb="NIH MGC 146"
/note="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file

ORIGIN

ftp://image.llnl.gov/image.rearrayed_plates/IRBF.presv.dat
a. Note: this is a NIH_MGC Library."

Query Match 69.8%; Score 693; DB 7; Length 720;
Best Local Similarity 99.9%; Pred. No. 3e-190;
Matches 704; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 288 GATTATGCTTATTCCTGATGCAACATGATGACAGATATTTATTTCTGACCCGCT 347
DB 720 GATTATGCTTATTCCTGATGCAACATGATGACAGATATTTATTTCTGACCCGCT 661
QY 348 GAGTGTGTCGCTTCTGCAATGATTCACCCCTTCGCTTCGATGTCACAGCAT 407
DB 660 GAGTGTGTCGCTTCTGCAATGATTCACCCCTTCGCTTCGATGTCACAGCAT 601
QY 408 CAGAGTGCCTGATTCCTGTCGATGATGATGATGATGATGATGATGATGATGAT 467
DB 600 CAGAGTGCCTGATTCCTGTCGATGATGATGATGATGATGATGATGATGATGAT 541
QY 468 GCTCTGAGAGTGCCTGTCAGAGAACGGCAGATGTCATCATGCTTAAGCTGATCT 527
DB 540 GCTCTGAGAGTGCCTGTCAGAGAACGGCAGATGTCATCATGCTTAAGCTGATCT 481
QY 528 CTATTAATATGCTTAAGTGCAGACCATGATATATTCCTGTCGTCGCTGCT 587
DB 480 CTATTAATATGCTTAAGTGCAGACCATGATATATTCCTGTCGTCGCTGCT 421
QY 588 GCCATTTTCACTCAGCATCTGTTATCTGTCGATCATTCGCGTTCTGTTAAAGTGA 647
DB 420 GCCATTTTCACTCAGCATCTGTTATCTGTCGATCATTCGCGTTCTGTTAAAGTGA 361
QY 648 GGTCCAGATGCGGGGCTGCGGTTCTCAGAGAGGCACTGACCACTCATCTCATC 707
DB 360 GGTCCAGATGCGGGGCTGCGGTTCTCAGAGAGGCACTGACCACTCATCTCATC 301
QY 708 CTATGATCATCTTCTTCTGTTTCTGTCGCTTATCACTCAGTACGCTGCTGAC 767
DB 300 CTATGATCATCTTCTTCTGTTTCTGTCGCTTATCACTCAGTACGCTGCTGAC 241
QY 768 GATATGGAAGTGGTTTATGCAAGACAGATGCAATTAAGCTTTGTTATCACTGCG 827
DB 240 GATATGGAAGTGGTTTATGCAAGACAGATGCAATTAAGCTTTGTTATCACTGCG 181
QY 828 CTGAGCAGAGCCATGCTGCTTCAATCCTGCTCTATTACTTTGCTGGGAGATTT 887
DB 180 CTGAGCAGAGCCATGCTGCTTCAATCCTGCTCTATTACTTTGCTGGGAGATTT 121
QY 888 TAAAGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCACAGAGGCAAGCAAGTG 947
DB 120 TAAAGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCACAGAGGCAAGCAAGTG 61
QY 948 TGTTCCTCTGTTAGTGTGTGTTGAGAAAGCAAGAGTATA 992
DB 60 TGTTCCTCTGTTAGTGTGTGTTGAGAAAGCAAGAGTATA 17

RESULT 2

LOCUS CD630086 758 bp mRNA linear EST 12-JAN-2004
DEFINITION 5604002J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630086
VERSION CD630086.1 GI:40278352
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Fu G.-K., Wang J.-T., Yang J., Au-Young J. and Seuve L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)

COMMENT

Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES

source

1..758
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_11b="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 68.0%; Score 675; DB 6; Length 758;
Best Local Similarity 98.9%; Pred. No. 5.4e-185;
Matches 701; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 1 ATGGAACCAATGGGACCTTCAGCAATTAACAAGAGGAACTGCAATTAAGAACTTC 60
DB 50 ATGGAACCAATGGGACCTTCAGCAATTAACAAGAGGAACTGCAATTAAGAACTTC 109
QY 61 AAGAGGAATTTTCCATTTGATATCTGATATATTTTCTGGGAGTCTTGGGAAT 120
DB 110 AAGAGGAATTTTCCATTTGATATCTGATATATTTTCTGGGAGTCTTGGGAAT 169
QY 121 GGGTGTCCATATATGTTTCTTCGACGCTTATTAAGAGTCCATCTGTGAAGTTTTC 180
DB 170 GGGTGTCCATATATGTTTCTTCGACGCTTATTAAGAGTCCATCTGTGAAGTTTTC 229
QY 181 ATGCTAAATCTGGCCATTTCAATCTCCTGTTATTAAGAGCTTCCTTCAGGGCTGAC 240
DB 230 ATGCTAAATCTGGCCATTTCAATCTCCTGTTATTAAGAGCTTCCTTCAGGGCTGAC 289
QY 241 TATTAATCTTAAGAGCTTCAATTTGATATTTTGGAGACTGCTGAGATTAATGTTTAT 300
DB 290 TATTAATCTTAAGAGCTTCAATTTGATATTTTGGAGACTGCTGAGATTAATGTTTAT 349
QY 301 TCCCTGTATGTAACATGATGACAGATTTTATTTTCCCTGACCGTGTAGTGTGTGCT 360
DB 350 TCCCTGTATGTAACATGATGACAGATTTTATTTTCCCTGACCGTGTAGTGTGTGCT 409
QY 361 TTCCTGCAATAGTTTCAACCCCTTTCGCTTCGATGTCACAGAGATGAGAGTCTGAG 420
DB 410 TTCCTGCAATAGTTTCAACCCCTTTCGCTTCGATGTCACAGAGATGAGAGTCTGAG 469
QY 421 ATCTCTGTGGATCATATGATATGATTCCTTAATGCTTCCTCAATATGCTCTGAGACGT 480
DB 470 ATCTCTGTGGATCATATGATATGATTCCTTAATGCTTCCTCAATATGCTCTGAGACGT 529
QY 481 GGCCTGAGCAAGACGGAGTGTCACTCATGCTTAAGCTGAATCTCTATTAATTTGCT 540
DB 530 GGCCTGAGCAAGACGGAGTGTCACTCATGCTTAAGCTGAATCTCTATTAATTTGCT 589
QY 541 AAGCTGACAGCAATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
DB 590 AAGCTGACAGCAATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 649
QY 600 ACTGAGCATCTGTTATCTGCTGATCATTCGAGTTCCTGTTAAAGTGAAGTCCAGGAATC 659
DB 650 ACTGAGCATCTGTTATCTGCTGATCATTCGAGTTCCTGTTAAAGTGAAGTCCAGGAATC 709
QY 660 GGGGCTGC--GGGTTTCAAGAGGACCTGACCAACATCATCATCA 706
DB 710 GGGGCTGCAGGGTTCCTCAGAGAGGACCTGACCAACATCATCATCA 758

RESULT 3

LOCUS CD630084 762 bp mRNA linear EST 12-JAN-2004
DEFINITION 56040024J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630084
VERSION CD630084.1 GI:40278350

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 762)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
FEATURES
source 1..762
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
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Query Match 67.1%; Score 666; DB 6; Length 762;
Best Local Similarity 99.4%; Pred. No. 2.3e-182;
Matches 700; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
QY 1 ATGGAACCAATGCGACCTTCAGCATATACACAGAGAACTGCACAAATGAAAATTTC 60
DB 50 ATGGAACCAATGCGACCTTCAGCATATACACAGAGAACTGCACAAATGAAAATTTC 109
QY 61 AAGAGAAATTTTCCCAATGTATATCTGATATATTTTTCGGGAGTCTTGGGAAT 120
DB 110 AAGAGAAATTTTCCCAATGTATATCTGATATATTTTTCGGGAGTCTTGGGAAT 169
QY 121 GGGTGTCCATATATGTTTCCGAGCCTTATAGAACTGCACAACTGGAACGTTTC 180
DB 170 GGGTGTCCATATATGTTTCCGAGCCTTATAGAACTGCACAACTGGAACGTTTC 229
QY 181 ATGTAATCTGGCCATTCAGATCTCTGTCATTAAGACGCTTCCTTCAGGGCTGAC 240
DB 230 ATGTAATCTGGCCATTCAGATCTCTGTCATTAAGACGCTTCCTTCAGGGCTGAC 289
QY 241 TATTAATCTTAAGAGCTCCAAATGTGATATTTGAGACCTGCGCTGAGATATGCTTAT 300
DB 290 TATTAATCTTAAGAGCTCCAAATGTGATATTTGAGACCTGCGCTGAGATATGCTTAT 349
QY 301 TCCTGTATGTAACATGTAAGCACTATTTTCCCTGACCGTGTGATGTTGCGT 360
DB 350 TCCTGTATGTAACATGTAAGCACTATTTTCCCTGACCGTGTGATGTTGCGT 409
QY 361 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCGATGTCACAGCATCAGAGTGGCTGG 420
DB 410 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCGATGTCACAGCATCAGAGTGGCTGG 469
QY 421 ATCTCTGTGGATCATATATGATCTTATCATGGCTTCCTCAATAATGCTTCCTGACAGT 480
DB 470 ATCTCTGTGGATCATATATGATCTTATCATGGCTTCCTCAATAATGCTTCCTGACAGT 529
QY 481 GGCTCTGAGCAGAAAGGAGGTGTCAATCATGCTTAAGACTGAATCTCTAATAATTTGCT 540
DB 530 GGCTCTGAGCAGAAAGGAGGTGTCAATCATGCTTAAGACTGAATCTCTAATAATTTGCT 589
QY 541 AAGCTGACAGACCATGAACTATATTTGCTTGGTGGGCTGGCC-TGCTGCAATTTTTCAC 599
DB 590 AAGCTGACAGACCATGAACTATATTTGCTTGGTGGGCTGGCC-TGCTGCAATTTTTCAC 649
QY 600 ACTCAGACATCTTATCTGCTGATCATTTGGGGTCTGTATA-AAAGTGAGGT-CCGAGA 656
DB 650 ACTCAGACATCTTATCTGCTGATCATTTGGGGTCTGTATA-AAAGTGAGGT-CCGAGA 709
QY 657 ATCGGGGCTGGGGTTTCTCAGAGAAAGCAGTGCACCAACATCA 700

DB 710 ATCGGGGCTGGGGTTTCTCAGAGAAAGCAGTGCACCAACATCA 753
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RESULT 4 CD630072 745 bp mRNA linear EST 12-JUN-2004
LOCUS 56039924J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630072
ACCESSION CD630072.1 GI:40278338
VERSION CD630072.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 745)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
FEATURES
source 1..745
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
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Query Match 66.8%; Score 663; DB 6; Length 745;
Best Local Similarity 99.7%; Pred. No. 1.7e-181;
Matches 665; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 ATGGAACCAATGCGACCTTCAGCATATACACAGAGAACTGCACAAATGAAAATTTC 60
DB 50 ATGGAACCAATGCGACCTTCAGCATATACACAGAGAACTGCACAAATGAAAATTTC 109
QY 61 AAGAGAAATTTTCCCAATGTATATCTGATATATTTTTCGGGAGTCTTGGGAAT 120
DB 110 AAGAGAAATTTTCCCAATGTATATCTGATATATTTTTCGGGAGTCTTGGGAAT 169
QY 121 GGGTGTCCATATATGTTTCCGAGCCTTATAGAACTGCACAACTGGAACGTTTC 180
DB 170 GGGTGTCCATATATGTTTCCGAGCCTTATAGAACTGCACAACTGGAACGTTTC 229
QY 181 ATGTAATCTGGCCATTCAGATCTCTGTCATTAAGACGCTTCCTTCAGGGCTGAC 240
DB 230 ATGTAATCTGGCCATTCAGATCTCTGTCATTAAGACGCTTCCTTCAGGGCTGAC 289
QY 241 TATTAATCTTAAGAGCTCCAAATGTGATATTTGAGACCTGCGCTGAGATATGCTTAT 300
DB 290 TATTAATCTTAAGAGCTCCAAATGTGATATTTGAGACCTGCGCTGAGATATGCTTAT 349
QY 301 TCCTGTATGTAACATGTAAGCACTATTTTCCCTGACCGTGTGATGTTGCGT 360
DB 350 TCCTGTATGTAACATGTAAGCACTATTTTCCCTGACCGTGTGATGTTGCGT 409
QY 361 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCGATGTCACAGCATCAGAGTGGCTGG 420
DB 410 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCGATGTCACAGCATCAGAGTGGCTGG 469
QY 421 ATCTCTGTGGATCATATATGATCTTATCATGGCTTCCTCAATAATGCTTCCTGACAGT 480
DB 470 ATCTCTGTGGATCATATATGATCTTATCATGGCTTCCTCAATAATGCTTCCTGACAGT 529
QY 481 GGCTCTGAGCAGAAAGGAGGTGTCAATCATGCTTAAGACTGAATCTCTAATAATTTGCT 540
DB 530 GGCTCTGAGCAGAAAGGAGGTGTCAATCATGCTTAAGACTGAATCTCTAATAATTTGCT 589

Qy	541	AAGCTGACACCATGAACTATATTTGGCTTGATGG-7GGGCTGCTGCTGGCATTTTTCAC	593
Db	590	AAGCTGACACCATGAACTATATTTGGCTTGATGG-7GGGCTGCTGCTGGCATTTTTCAC	649
Qy	600	ACTCAGACATCTGTATCTGCTGATCAATTCGGGTTCTGTAA-AGTAGAGTCCAGAAAT	658
Db	650	ACTCAGACATCTGTATCTGCTGATCAATTCGGGTTCTGTAA-AGTAGAGTCCAGAAAT	709
Qy	659	CGGGGCTGGGGTTTCTCAGAGAGG	685
Db	710	CGGGGCTGGGGTTTCTCAGAGAGG	736
RESULT 5			
LOCUS	CD630089	726 bp	mRNA linear
DEFINITION	56040096H1 FLP Homo sapiens cDNA, mRNA sequence.		EST 12-JAN-2004
ACCESSION	CD630089		
VERSION	CD630089.1	GI:40278355	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 726)		
TITLE	Fu, G.-K., Wang, J.-T., Yang, J.-, Au-Young, J., and Struve, L. L.		
JOURNAL	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes		
COMMENT	Genomics 84 (1), 205-210 (2004)		
	Contact: Fu GK		
	Incyte Genomics, Inc.		
	3160 Porter Dr., Palo Alto, CA 94304, USA		
	Tel: 6508454102		
	Email: gfu@incyte.com.		
FEATURES			
source	Location/Qualifiers		
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	/organism="Homo sapiens"		
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	/db_xref="taxon:9606"		
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Query Match	66.6%;	Score 661.2;	DB 6;
Best Local Similarity	99.4%;	Pred. No. 5.6e-181;	
Matches	674;	Conservative	0; Mismatches 3; Indels 1; Gaps 1;
Qy	1	ATGGAACCAATGGACCTTCAGCAATTAACAACAGACAGAACTGCACATTTGAAAATTC	60
Db	50	ATGGAACCAATGGACCTTCAGCAATTAACAACAGACAGAACTGCACATTTGAAAATTC	109
Qy	61	AAGAGAGAAATTTTCCAAATGTATATCTGATTAATTTTCTGGGGAGTCTTGGGAAAT	120
Db	110	AAGAGAGAAATTTTCCCAATGTATATCTGATTAATTTTCTGGGGAGTCTTGGGAAAT	169
Qy	121	GGGTTTCATATATATGTTTCTCGAGCCTTATAAGAAATCCACATCTGTGAACGTTTC	180
Db	170	GGGTTTCATATATATGTTTCTCGAGCCTTATAAGAAATCCACATCTGTGAACGTTTC	229
Qy	181	ATGCTAAATCTGGGCATTTCCAGATATCTCTGTTCATTAAGCAGCTTCCCTTAGGGCTGAC	240
Db	230	ATGCTAAATCTGGGCATTTCCAGATATCTCTGTTCATTAAGCAGCTTCCCTTAGGGCTGAC	289
Qy	241	TATATCTTAGAGGCTCCAAATTTGATATTTTGGAGACCTGGCTGAGGATTAATGCTTAT	300
Db	290	TATATCTTAGAGGCTCCAAATTTGATATTTTGGAGACCTGGCTGAGGATTAATGCTTAT	349
Qy	301	TCTTTGATGTCACATGTACAGCAGATATTTATTTCTGACCGTGTGAGTGTGCGT	360
Db	350	TCTTTGATGTCACATGTACAGCAGATATTTATTTCTGACCGTGTGAGTGTGCGT	409
Qy	361	TTCCGTGGAAATGATCACCCCTTTTCGGTTCTGATGTACACAGATTCAGAGATGCTCG	420

Db	410	TTCTCGGCAATGGTTCACCCCTTTGGCTTCTGATGTGACACAGATACAGAGTCCCTGG	465
Qy	421	ATCTCTGTGGGATCATATAGATTCCTTATTCATAGGCTCTCTCAATATATGCTCTCGACAGT	480
Db	470	ATCTCTGTGGGATCATATAGATTCCTTATTCATAGGCTCTCTCAATATATGCTCTCGACAGT	529
Qy	481	GGCTCTGAGCAGGAACGGAGTGTCACATCATAGCTTAGAGCTGAATCTCTATTAATTTGCT	540
Db	530	GGCTCTGAGCAGGAACGGAGTGTCACATCATAGCTTAGAGCTGAATCTCTATTAATTTGCT	589
Qy	541	AAGCTGCAGACCATGAACCTATATTTGCCCTTGGTGGTGGGCTGCTGCTGCCATTTTTCACA	600
Db	590	AAGCTGCAGACCATGAACCTATATTTGCCCTTGGTGGTGGGCTGCTGCTGCCATTTTTCACA	648
Qy	601	CTCAGCATCTGTATCTGCTGATCATTTGGGTTCTGTTAAAAGTGAGAGTCCCAAGATCG	660
Db	649	CTCAGCATCTGTATCTGCTGATCATTCGGGTTGGGTTAAAAGTGAGAGTCCCAAGATCG	708
Qy	661	GGGCTGGCGGGTTTCTCAC	678
Db	709	GGGCTGGCGGGTTTCTCAC	726
RESULT 6			
LOCUS	CD630075	753 bp	mRNA linear EST 12-JAN-2004
DEFINITION	56039988H1 FLP Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD630075		
VERSION	CD630075.1	GI:40278341	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 753)		
TITLE	Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.J.		
JOURNAL	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes		
COMMENT	Genomics 84 (1), 205-210 (2004)		
CONTACT	Contact: Fu GK		
INCYTE	Incyte Genomics, Inc.		
PORTER	3160 Porter Dr., Palo Alto, CA 94304, USA		
TEL	Tel: 6508454102		
EMAIL	Email: gfu@incyte.com.		
FEATURES	Location/Qualifiers		
SOURCE	1..753		
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	/clone_lib="FLP"		
	/note="Vector: pDrive Cloning Vector"		
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Query Match	63.6%;	Score 632;	DB 6;
Best Local Similarity	98.3%;	Pred. No. 1.8e-172;	
Matches 692;	Conservative 0;	Mismatches 5;	Indels 7;
Gaps	5;		
Qy	1	ATGGAACCAATATGGACCTTCAGCAATTAACAACAGCAGCAATCGCAATTTGAAACTTC	60
Db	50	ATGGAACCAATATGGACCTTCAGCAATTAACAACAGCAGCAATCGCAATTTGAAACTTC	109
Qy	61	AAGAGAGATTTTCCCAATTTGTATATCTGATATATTTTCTGGGAGTCTTGGGAAAT	120
Db	110	AAGAGAGATTTTCCCAATTTGTATATCTGATATATTTTCTGGGAGTCTTGGGAAAT	169
Qy	121	GGGTTGTCATATATGTTTTCTGCAAGCTTATPAAGAGTCCACATCTGGAACGTTTTTC	180
Db	170	GGGTTGTCATATATGTTTTCTGCAAGCTTATPAAGAGTCCACATCTGGAACGTTTTTC	229
Qy	181	ATGCTAAATCTGGCAATTTGAGATCTCTGTTGATATAGACAGCTTCCCTCAAGGGCTGAC	240
Db	230	ATGCTAAATCTGGCAATTTGAGATCTCTGTTGATATAGACAGCTTCCCTCAAGGGCTGAC	289

QY 241 TATTATCTAGAGGCTCAATTGATATTGAGACCTGGCCGAGATATGCTTAT 300
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Db 290 TATTATCTTAGAGGCTCAATTGATATTGAGACCTGGCCGAGATATGCTTAT 349
| | | | |
QY 301 TCCCTGTATGTCAACATGTACAGAGATATTATTTCTGACCGTGTGATGTGCGT 360
| | | | |
Db 350 TCCCTGTATGTCAACATGTACAGAGATATTATTTCTGACCGTGTGATGTGCGT 409
| | | | |
QY 361 TCCCTGTGCAATGTTCAACCCCTTTGGGCTTGTGATGTCAACAGCATCAGAGTGTCTGG 420
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Db 410 TTCTGTGGCAATGTTCAACCCCTTTGGGCTTGTGATGTCAACAGCATCAGAGTGTCTGG 469
| | | | |
QY 421 ATCTCTGTGGGATCATATGATATCTTATCATGGGCTTCTCAATAATGCTCCGAGCACT 480
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Db 470 ATCTCTGTGGGATCATATGATATCTTATCATGGGCTTCTCAATAATGCTCCGAGCACT 529
| | | | |
QY 481 GGCTCTGAGCAGAACGGCAGTGTCAATCATGATGCTTAGAGCTGATCTTA-TAAATTGC 539
| | | | |
Db 530 GGCTCTGAGCAGAACGGCAGTGTCAATCATGATGCTTAGAGCTGATCTTA-TAAATTGC 589
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QY 540 TTAGCTGCAGACCATGATATATTTGCTTGTGTGCTGGCTGCTGCTGCA-TTTTCA 598
| | | | |
Db 590 TTAGCTGCAGACCATGATATATTTGCTTGTGTGCTGGCTGCTGCTGCA-TTTTCA 649
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QY 599 CACTGAGCATCTGTATCTG-CTGATCATTTGGGCTTGTGTAAGTGAAGTCCAGAA 657
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Db 650 CACTGAGCATCTGTATCTGCTGATCATTTGGGCTTGTGTAAGTGAAGT-CCAGAA 708
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QY 658 TCGGGGCTGGGGTTCTC--ACAGGAAGCAGTACCAACAT 698
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Db 709 TCGGGGCTGGGGTTCTCCTCACAGGAAGCAGTACCAACAT 752
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RESULT 7
CD630077 750 bp mRNA linear EST 12-JAN-2004
LOCUS 56039996H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630077
ACCESSION CD630077.1 GI:40278343
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 750)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
Source
1..750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1fb="FLP"
/note="Vector: pDrive Cloning Vector"
ORIGIN
Query Match 62.4%; Score 619.2; DB 6; Length 750;
Best Local Similarity 97.3%; Pred. No. 9, 8e-169;
Matches 683; Conservative 0; Mismatches 13; Indels 6; Gaps 5;
1 ATGGAACCAATGGGACCTTCAAGCAATTAACAACAGCAGAACTGCACAACTGAAAACTTC 60
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Db 50 ATGGAACCAATGGGACCTTCAAGCAATTAACAACAGCAGAACTGCACAACTGAAAACTTC 109
| | | | |
QY 61 AAGAGAGATTTTCCCAATGTATATCTGATTAATTTTTCGGGGAGCTTGGGAAT 120
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Db 110 AAGAGAGATTTTCCCAATGTATATCTGATTAATTTTTCGGGGAGCTTGGGAAT 169
| | | | |
QY 121 GGGTGTCCATATATATTTTCTCGACGCTTAATAAGATCCACATCTGTGAACGTTTTC 180
| | | | |
Db 170 GGGTGTCCATATATATTTTCTCGACGCTTAATAAGATCCACATCTGTGAACGTTTTC 229
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QY 181 AAGCAATATCGGCATTTCAATCTCGTTCATTAAGAGGCTTCCCTCAAGGCTGAC 240
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Db 230 ATGCAATATCGGCATTTCAATCTCGTTCATTAAGAGGCTTCCCTCAAGGCTGAC 289
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QY 241 TATTATCTTAGAGGCTCCAAATTGATATTGAGACCTGGCCGAGATATGCTTAT 300
| | | | |
Db 290 TATTATCTTAGAGGCTCCAAATTGATATTGAGACCTGGCCGAGATATGCTTAT 349
| | | | |
QY 301 TCCCTGTATGTCAACATGTACAGAGATATTATTTCTGACCGTGTGATGTGCGT 360
| | | | |
Db 350 TCCCTGTATGTCAACATGTACAGAGATATTATTTCTGACCGTGTGATGTGCGT 409
| | | | |
QY 361 TTCTGTGGCAATGTTCAACCCCTTTGGGCTTGTGATGTCAACAGCATCAGAGTGTCTGG 420
| | | | |
Db 410 TTCTGTGGCAATGTTCAACCCCTTTGGGCTTGTGATGTCAACAGCATCAGAGTGTCTGG 469
| | | | |
QY 421 ATCTCTGTGGGATCATATGATATCTTATCATGGCTTCTCAATAATGCTCCGAGCACT 480
| | | | |
Db 470 ATCTCTGTGGGATCATATGATATCTTATCATGGCTTCTCAATAATGCTCCGAGCACT 529
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| | | | |
Db 490 GGCTCTGAGCAGAACGGCAGTGTCA-TCATCTTAGAGCTGAATCTCTAATAAATTGC 589
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QY 590 TAAAGCTGAGACCATGATATATTTGCTTGTGTGCTGGCTGCTGCTGCAATTTTCA 648
| | | | |
Db 599 CACTGAGCATCTGTATCTGATCATTTGGGCTTGTGTAAGTGAAGTCCAGAA 657
| | | | |
QY 649 AACTGAGCATCTGTATCTGCTGATCTTGGGCTTGTGTAAGTGAAGTCCAGAA 708
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QY 658 TCGGGGCTGGGG--TTTCTCACAGGAAGCAGTACCAACA 697
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Db 709 TCGGGGCTGGGGGTTTCTCACAGGAAGCAGTACCAACA 750
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RESULT 8
CD630069 673 bp mRNA linear EST 12-JAN-2004
LOCUS 56039916H1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD630069
ACCESSION CD630069.1 GI:40278335
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 673)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
Source
1..673
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1fb="FLP"
/note="Vector: pDrive Cloning Vector"
ORIGIN
Query Match 62.4%; Score 619.2; DB 6; Length 750;
Best Local Similarity 97.3%; Pred. No. 9, 8e-169;
Matches 683; Conservative 0; Mismatches 13; Indels 6; Gaps 5;
1 ATGGAACCAATGGGACCTTCAAGCAATTAACAACAGCAGAACTGCACAACTGAAAACTTC 60
| | | | |
Db 50 ATGGAACCAATGGGACCTTCAAGCAATTAACAACAGCAGAACTGCACAACTGAAAACTTC 109
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QY 61 AAGAGAGATTTTCCCAATGTATATCTGATTAATTTTTCGGGGAGCTTGGGAAT 120
| | | | |

ORIGIN
Query Match 62.4%; Score 619.2; DB 6; Length 750;
Best Local Similarity 97.3%; Pred. No. 9, 8e-169;
Matches 683; Conservative 0; Mismatches 13; Indels 6; Gaps 5;
1 ATGGAACCAATGGGACCTTCAAGCAATTAACAACAGCAGAACTGCACAACTGAAAACTTC 60
| | | | |
Db 50 ATGGAACCAATGGGACCTTCAAGCAATTAACAACAGCAGAACTGCACAACTGAAAACTTC 109
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QY 61 AAGAGAGATTTTCCCAATGTATATCTGATTAATTTTTCGGGGAGCTTGGGAAT 120
| | | | |

Query Match 62.2%; Score 618; DB 6; Length 673;
 Best Local Similarity 100.0%; Pred. No. 2.1e-168;
 Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAACCAATGGACCTTCAGCAATTAACAAGCAAGCAAGCAATTCGCAATTTGAAACTTC 60
 DB 50 ATGGAACCAATGGACCTTCAGCAATTAACAAGCAAGCAAGCAATTCGCAATTTGAAACTTC 109
 QY 61 AAGAGAAATTTTCCCAATTTATCTGATATATTTTTCGGGAGCTTGGGAAAT 120
 DB 110 AAGAGAAATTTTCCCAATTTATCTGATATATTTTTCGGGAGCTTGGGAAAT 169
 QY 121 GGGTTCATATATGTTTTCCTGACAGCTTATTAAGAAGTCCATCTGGAAGTTTC 180
 DB 170 GGGTTCATATATGTTTTCCTGACAGCTTATTAAGAAGTCCATCTGGAAGTTTC 229
 QY 181 ATGCTAAATCTGGGCAATTCAGATCTCTGTTCAATAGCAAGCTTCCTTCAGGGCTGAC 240
 DB 230 ATGCTAAATCTGGGCAATTCAGATCTCTGTTCAATAGCAAGCTTCCTTCAGGGCTGAC 289
 QY 241 TATTATCTTAGAGCTTCATTTGATATTGAGACCTGGCTGCAAGATTATGCTTAT 300
 DB 290 TATTATCTTAGAGCTTCATTTGATATTGAGACCTGGCTGCAAGATTATGCTTAT 349
 QY 301 TCCCTGATGTCAACATGTACAGAGATTTATTTCCCTGACGGGTGAGTGTGCGT 360
 DB 350 TCCCTGATGTCAACATGTACAGAGATTTATTTCCCTGACGGGTGAGTGTGCGT 409
 QY 361 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCGATGTCAACAGCATCAGAGATGCTG 420
 DB 410 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCGATGTCAACAGCATCAGAGATGCTG 469
 QY 421 ATCCCTGTGGGATCTATAGGATTCCTTATATAGGCTTTCCTCAATATGCTCTGACAGT 480
 DB 470 ATCCCTGTGGGATCTATAGGATTCCTTATATAGGCTTTCCTCAATATGCTCTGACAGT 529
 QY 481 GGCTGTAGAGCAAGCGAGTGTCAATCATGCTTGAAGTGAATCTTAATAAATGCT 540
 DB 530 GGCTGTAGAGCAAGCGAGTGTCAATCATGCTTGAAGTGAATCTTAATAAATGCT 589
 QY 541 AAGCTGCAAGCAATGATATATGCTTGTGTGTGGCTGCTGCTGCAATTTTCA 600
 DB 590 AAGCTGCAAGCAATGATATATGCTTGTGTGTGGCTGCTGCTGCAATTTTCA 649
 QY 601 CTCAGCATCTTATCTG 618
 DB 650 CTCAGCATCTTATCTG 667

RESULT 9
 CO959148 729 bp mRNA linear EST 17-AUG-2004
 LOCUS AGENCOURT_30842618 NIH_MGC_146 Homo sapiens cDNA clone
 DEFINITION IMAGE:7389737 5', mRNA sequence.

ACCESSION CO959148
 VERSION CO959148.1 GI:51323730
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 729)
 NIH-MGC <http://mgs.nci.nih.gov/>
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Guthrie cDNA Resource Center
 CDNA Library Preparation: Guthrie cDNA Resource Center

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 plate: IRB17 row: f column: 03
 High quality sequence stop: 602.
 Location/Qualifiers

FEATURES

source

1..729

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:7389737"

/tissue_type="mixed"

/lab_host="DH10B (T1-phage-resistant)"

/clone_id="NIH_MGC_146"

/note="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cdna)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
[ftp://image.llnl.gov/image_retrieval_plates/IRBF.presv.dat](http://image.llnl.gov/image_retrieval_plates/IRBF.presv.dat)
a. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 61.1%; Score 607.2; DB 7; Length 729;
 Best Local Similarity 94.7%; Pred. No. 3e-165;
 Matches 648; Conservative 0; Mismatches 32; Indels 4; Gaps 2;

QY 1 ATGGAACCAATGGACCTTCAGCAATTAACAAGCAAGCAATTCGCAATTTGAAACTTC 60
 DB 50 ATGGAACCAATGGACCTTCAGCAATTAACAAGCAAGCAAGCAATTCGCAATTTGAAACTTC 109
 QY 61 AAGAGAAATTTTCCCAATTTATCTGATATATTTTTCGGGAGCTTGGGAAAT 120
 DB 110 AAGAGAAATTTTCCCAATTTATCTGATATATTTTTCGGGAGCTTGGGAAAT 169
 QY 121 GGGTTCATATATGTTTTCCTGACAGCTTATTAAGAAGTCCATCTGGAAGTTTC 180
 DB 170 GGGTTCATATATGTTTTCCTGACAGCTTATTAAGAAGTCCATCTGGAAGTTTC 229
 QY 181 ATCCCTGTGGGATCTATAGGATTCCTTATATAGGCTTTCCTCAATATGCTCTGACAGT 240
 DB 230 ATCCCTGTGGGATCTATAGGATTCCTTATATAGGCTTTCCTCAATATGCTCTGACAGT 289
 QY 241 TATTATCTTAGAGCTTCATTTGATATTGAGACCTGGCTGCAAGATTATGCTTAT 300
 DB 290 TATTATCTTAGAGCTTCATTTGATATTGAGACCTGGCTGCAAGATTATGCTTAT 349
 QY 301 TCCCTGATGTCAACATGTACAGAGATTTATTTCCCTGACGGGTGAGTGTGCGT 360
 DB 350 TCCCTGATGTCAACATGTACAGAGATTTATTTCCCTGACGGGTGAGTGTGCGT 409
 QY 361 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCGATGTCAACAGCATCAGAGATGCTG 420
 DB 410 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCGATGTCAACAGCATCAGAGATGCTG 469
 QY 421 ATCCCTGTGGGATCTATAGGATTCCTTATATAGGCTTTCCTCAATATGCTCTGAGAGT 480
 DB 470 ATCCCTGTGGGATCTATAGGATTCCTTATATAGGCTTTCCTCAATATGCTCTGAGAGT 529
 QY 481 GGCTGTAGAGCAAGCGAGTGTCAATCATGCTTGAAGTGAATCTTAATAAATGCT 540
 DB 530 GGCTGTAGAGCAAGCGAGTGTCAATCATGCTTGAAGTGAATCTTAATAAATGCT 589
 QY 541 AAGCTGCAAGCAATGATATATGCTTGTGTGTGGCTGCTGCTGCAATTTTCA 600
 DB 590 AAGCTGCAAGCAATGATATATGCTTGTGTGTGGCTGCTGCTGCAATTTTCA 648
 QY 601 CTCAGCATCTTATCTGATCATTCGGGTTCTGTTAAAGAAGTGAAGTCCCAAGATCG 660

Db 649 CTCAGACCTCTGATCTGCTGATCATTCGGTTCCTTAATAATGAAG---TCNGAATC 705
Qy 661 GGGCTGCGGGGTTTCTGACAGGAG 684
Db 706 NNGCTGCGGGTTTCACAAAGAAAG 729

RESULT 10
CD630079 652 bp mRNA linear EST 12-JAN-2004
LOCUS 56040008H1 FLP Homo sapiens cDNA, mRNA sequence.
CD630079
ACCESSION CD630079.1 GI:40278345
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
DEFINITION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Pu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
Genomics 84 (1), 205-210 (2004)
JOURNAL
COMMENT Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
source 1..652
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1fb="FLP"
/note="Vector: pDrive Cloning Vector"

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Query Match 60.7%; Score 603; DB 6; Length 652;
Best Local Similarity 100.0%; Pred. No. 4.9e-164;
Matches 603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGAACCAATGGGACCTTGACGATATACACAGCAGCACTGCAATGAAAATTTC 60
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50 ATGGAACCAATGGGACCTTGACGATATACACAGCAGCACTGCAATGAAAATTTC 109
|||||
61 AAGAGAGATTTTCCCAATGTATATCTGATTAATTTTCTGGGAGCTCTTGGGAAT 120
|||||
110 AAGAGAGATTTTCCCAATGTATATCTGATTAATTTTCTGGGAGCTCTTGGGAAT 169
|||||
121 GGGTGTCCATATATATGTTTCTCTGACGCTTAAAGAGTCAATCTGTGAACGTTTTT 180
|||||
170 GGGTGTCCATATATATGTTTCTCTGACGCTTAAAGAGTCAATCTGTGAACGTTTTT 229
|||||
181 ATGCTAAATCTGGCAATTCAGATCTCGTTCAATAGACGCTTCCCTGAGGGGTGAC 240
|||||
220 ATGCTAAATCTGGCAATTCAGATCTCGTTCAATAGACGCTTCCCTGAGGGGTGAC 289
|||||
241 TATTAATCTTAGAGGCTCCAAATGATATTTGGAGACTGGCTGAGAAATATGCTTAAT 300
|||||
290 TATTAATCTTAGAGGCTCCAAATGATATTTGGAGACTGGCTGAGAAATATGCTTAAT 349
|||||
301 TCTTGTATGTACAATGATGACAGCATATTTATTTCTGACCGTGTGATGTTGTGCT 360
|||||
350 TCTTGTATGTACAATGATGACAGCATATTTATTTCTGACCGTGTGATGTTGTGCT 409
|||||
361 TTCCTGGCAATGAGTTCACCCCTTGGGCTTGGCAATGTACACAGCACTCAAGAGTGCTGG 420
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410 TTCCTGGCAATGAGTTCACCCCTTGGGCTTGGCAATGTACACAGCACTCAAGAGTGCTGG 469
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421 ATCTCTGTGGATCATATGATATCTTATCATGAGCTTCTCTCAATATATGCTCTGAGCAAT 480
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470 ATCTCTGTGGATCATATGATATCTTATCATGAGCTTCTCTCAATATATGCTCTGAGCAAT 529
|||||

Qy 481 GGCTCGAGCAGAACGGGAGTGCATCATGCTTAGAGCTGATCTGTATTAATTTGCT 540
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Db 530 GGCTCGAGCAGAACGGGAGTGCATCATGCTTAGAGCTGATCTGTATTAATTTGCT 589
|||||
Qy 541 AAGCTGACAGACCATGATATATTCCTTGTGTGTGGGCTGCTGCAATTTTTCACA 600
|||||
Db 590 AAGCTGACAGACCATGATATATTCCTTGTGTGTGGGCTGCTGCAATTTTTCACA 649
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Qy 601 CTC 603
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Db 650 CTC 652

RESULT 11
CD630087 670 bp mRNA linear EST 12-JAN-2004
LOCUS 56040008H1 FLP Homo sapiens cDNA, mRNA sequence.
CD630087
ACCESSION CD630087.1 GI:40278353
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
DEFINITION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Pu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
JOURNAL
COMMENT Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
source 1..670
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1fb="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
Query Match 60.4%; Score 599.4; DB 6; Length 670;
Best Local Similarity 99.7%; Pred. No. 5.5e-163;
Matches 611; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

1 ATGGAACCAATGGGACCTTGACGATATACACAGCAGCACTGCAATGAAAATTTC 60
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50 ATGGAACCAATGGGACCTTGACGATATACACAGCAGCACTGCAATGAAAATTTC 109
|||||
61 AAGAGAGATTTTCCCAATGTATATCTGATTAATTTTCTGGGAGCTCTTGGGAAT 120
|||||
110 AAGAGAGATTTTCCCAATGTATATCTGATTAATTTTCTGGGAGCTCTTGGGAAT 169
|||||
121 GGGTGTCCATATATATGTTTCTCTGACGCTTAAAGAGTCAATCTGTGAACGTTTTT 180
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170 GGGTGTCCATATATATGTTTCTCTGACGCTTAAAGAGTCAATCTGTGAACGTTTTT 229
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181 ATGCTAAATCTGGCAATTCAGATCTCGTTCAATAGACGCTTCCCTGAGGGGTGAC 240
|||||
220 ATGCTAAATCTGGCAATTCAGATCTCGTTCAATAGACGCTTCCCTGAGGGGTGAC 289
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241 TATTAATCTTAGAGGCTCCAAATGATATTTGGAGACTGGCTGAGAAATATGCTTAAT 300
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290 TATTAATCTTAGAGGCTCCAAATGATATTTGGAGACTGGCTGAGAAATATGCTTAAT 349
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301 TCTTGTATGTACAATGATGACAGCATATTTATTTCTGACCGTGTGATGTTGTGCT 360
|||||
350 TCTTGTATGTACAATGATGACAGCATATTTATTTCTGACCGTGTGATGTTGTGCT 409
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361 TTCCTGGCAATGAGTTCACCCCTTGGGCTTGGCAATGTACACAGCACTCAAGAGTGCTGG 420
|||||

Db 230 ATGTAATCTGGCCATTGAGATCTCTGTTCAATAGACGGCTTCCTTACAGGGTGAC 289
Qy 241 TATTATCTTAGAGGCTCCCAATGGATATTTGGAGACCTGGCTGCAGATTAATGCTTAT 300
Db 290 TATTATCTTAGAGGCTCCCAATGGATATTTGGAGACCTGGCTGCAGATTAATGCTTAT 349
Qy 301 TCCTGTATGTAACATGATGAGAGAGATTTATTTCTGACCGTGTGAGTGTGAGCT 360
Db 350 TCCTGTATGTAACATGATGAGAGAGATTTATTTCTGACCGTGTGAGTGTGAGCT 409
Qy 361 TTCCTGGAATGATTCACCCCTTTCGCTTGCATGTCAGCAGCATCAGAGATGCTGCG 420
Db 410 TTCCTGGAATGATTCACCCCTTTCGCTTGCATGTCAGCAGCATCAGAGATGCTGCG 469
Qy 421 ATCTCTGTGGAGATCATATGATTCCTTATCATAGGCTTCTCAATATGCTCTGAGAGT 480
Db 470 ATCTCTGTGGAGATCATATGATTCCTTATCATAGGCTTCTCAATATGCTCTGAGAGT 529
Qy 481 GGCTGTGAGCAGAGCGGAGTGTGACATGATGCTTATGAGAGTGAATCTATAAATA--TTG 538
Db 530 GGCTGTGAGCAGAGCGGAGTGTGACATGATGCTTATGAGAGTGAATCTATAAATAATTC 589
Qy 539 CTAGCTGAGACATGATGATTAATTCCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 598
Db 590 CTAGCTGAGACATGATGATTAATTCCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 649
Qy 599 CACTGAGATCTGTTATCTGCTGATCATTCGGG 631
Db 650 ACCTCAGATCTGTTATCTGCTGATCATTCGGG 682

RESULT 14

CF147785 729 bp mRNA linear EST 25-JUL-2003
LOCUS AGENCOURT 14740183 NIH MGC 145 Homo sapiens cDNA clone
DEFINITION IMAGE:6971946 5', mRNA sequence.
ACCESSION CF147785
VERSION CF147785.1 GI:33244053
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 729)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: IRB102 row: f column: 05
High quality sequence stop: 659.
Location/Qualifiers

FEATURES

Source 1..729
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..mol_type="mRNA"
..db_xref="taxon:9606"
..clone="IMAGE:6971946"
..tissue_type="mixed"
..lab_host="DH108"
..clone_1b="NIH MGC 145"
..note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XbaI/XhoI-3',
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
http://image.llnl.gov/image/feareyed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

Query Match 56.9%; Score 565; DB 7; Length 729;
Best Local Similarity 100.0%; Pred. No. 6e-153;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGCAAAATGGACCTTGCAGATTAACAACAGAGAACTGCAGATTTGAAATCTTC 60
Db 165 ATGAGCAAAATGGACCTTGCAGATTAACAACAGAGAACTGCAGATTTGAAATCTTC 224
Qy 61 AAGAGAAATTTTCCCAATGATATCTGATTAATTTTCTGGGAGCTTTGGAAAT 120
Db 225 AAGAGAAATTTTCCCAATGATATCTGATTAATTTTCTGGGAGCTTTGGAAAT 284
Qy 121 GGCTGTGATATATGTTTCTGAGAGCTTATAAGAGTCCACATCTGTGAAGCTTTTC 180
Db 285 GGCTGTGATATATGTTTCTGAGAGCTTATAAGAGTCCACATCTGTGAAGCTTTTC 344
Qy 181 ATGTAATCTGGACATTCAGATCTCGTTCATAGAGAGCTTCCCTTACAGGGCTGAC 240
Db 345 ATGTAATCTGGACATTCAGATCTCGTTCATAGAGAGCTTCCCTTACAGGGCTGAC 404
Qy 241 TATTATCTTAGAGGCTCCCAATGGATATTTGGAGACCTGGCTGCAGATTAATGCTTAT 300
Db 405 TATTATCTTAGAGGCTCCCAATGGATATTTGGAGACCTGGCTGCAGATTAATGCTTAT 464
Qy 301 TCCTGTATGTAACATGATGAGAGATTTATTTCTGACCGTGTGAGTGTGAGCT 360
Db 465 TCCTGTATGTAACATGATGAGAGATTTATTTCTGACCGTGTGAGTGTGAGCT 524
Qy 361 TTCCTGGAATGATTCACCCCTTTCGCTTGCATGTCAGCAGCATCAGAGATGCTGCG 420
Db 525 TTCCTGGAATGATTCACCCCTTTCGCTTGCATGTCAGCAGCATCAGAGATGCTGCG 584
Qy 421 ATCTCTGTGGAGATCATATGATTCCTTATCATAGGCTTCTCAATATGCTCTGAGAGT 480
Db 585 ATCTCTGTGGAGATCATATGATTCCTTATCATAGGCTTCTCAATATGCTCTGAGAGT 644
Qy 481 GGCTGTGAGCAGAGCGGAGTGTGACATGATGCTTATGAGAGTGAATCTATAAATAATTC 540
Db 645 GGCTGTGAGCAGAGCGGAGTGTGACATGATGCTTATGAGAGTGAATCTATAAATAATTC 704
Qy 541 AAGCTGAGACCATGATTAATTTG 565
Db 705 AAGCTGAGACCATGATTAATTTG 729

RESULT 15

LOCUS CD630066 633 bp mRNA linear EST 12-JAN-2004
DEFINITION 56039816R6 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD630066
VERSION CD630066.1 GI:40278332
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 633)
AUTHORS Fu G.K., Wang J.T., Yang J., Au-Young J. and Stuve L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102

FEATURES Email: gfu@ncycr.com,
Location/Qualifiers
SOURCE 1. .633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 54.7%; Score 543; DB 6; Length 633;
Best Local Similarity 99.8%; Pred. No. 1.5e-146;
Matches 554; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 50 ATGGAACCAATGGACCTTCAGCAATACACAGCAGCACTGCACAAATTGAAACTTC 109
   |||||||
QY 61 AAGAGAAATTTTCCCAATGTATCTGATATATTTTCTGGGAGCTTGGGAAAT 120
   |||||||
Db 110 AAGAGAAATTTTCCCAATGTATCTGATATATTTTCTGGGAGCTTGGGAAAT 169
   |||||||
QY 121 GGGTGTCCATATATGTTTCTCGACGCTTATPAGAAATGCCATCTGTGAACGTTTC 180
   |||||||
Db 170 GGGTGTCCATATATGTTTCTCGACGCTTATPAGAAATGCCATCTGTGAACGTTTC 229
   |||||||
QY 181 ATGCTAATCTGGCAATTCAGATCTCTGTGATTAAGACGCTTCCCTCAGGCTGAC 240
   |||||||
Db 230 ATGCTAATCTGGCAATTCAGATCTCTGTGATTAAGACGCTTCCCTCAGGCTGAC 289
   |||||||
QY 241 TATTATCTTAGAGGCTCCAAATGGATAATTGAGACCTGGCTGCAGATTAATGCTTAT 300
   |||||||
Db 290 TATTATCTTAGAGGCTCCAAATGGATAATTGAGACCTGGCTGCAGATTAATGCTTAT 349
   |||||||
QY 301 TCCTTGATGTCAACATGTACACAGATTTATTTCTGACCGTGTGAGTGTGCGT 360
   |||||||
Db 350 TCCTTGATGTCAACATGTACACAGATTTATTTCTGACCGTGTGAGTGTGCGT 409
   |||||||
QY 361 TTCCTGCAATGGTCAACCCCTTGGGCTTCTGATGTCAACGACATCAGAGTGCCTG 420
   |||||||
Db 410 TTCCTGCAATGGTCAACCCCTTGGGCTTCTGATGTCAACGACATCAGAGTGCCTG 469
   |||||||
QY 421 ATCTCTGTGGGATCAATATGATCTTATCATGGCTTCTCAATTAATGCTCTGACAGT 480
   |||||||
Db 470 ATCTCTGTGGGATCAATATGATCTTATCATGGCTTCTCAATTAATGCTCTGACAGT 529
   |||||||
QY 481 GGCTGAGAGAAAGGAGAGTGTCAATCATATGCTTAGAGC-TGAATCTATTAATTTGC 539
   |||||||
Db 530 GGCTGAGAGAAAGGAGAGTGTCAATCATATGCTTAGAGCTTGAATCTTATTAATTTGC 589
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QY 540 TAAGCTGACAGCCAT 554
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Db 590 TAAGCTGACAGCCAT 604
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Search completed: March 20, 2005, 02:52:30
Job time : 3872.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2005, 11:53:02 ; Search time 44 Seconds
(without alignments)
721.626 Million cell updates/sec

Title: US-09-826-791a-2
Perfect score: 1712
Sequence: 1 MEPNGTFSNNSRNCTIENF.....KAKTKCVFPVSVMRKRETV 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 95%
Maximum Match 100%
Listing first 80 summaries

Database : PIR_79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description

No matches found

Search completed: April 1, 2005, 12:01:38
Job time : 44 secs

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